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(without alignments)
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | Description | Novel signal trans | Human ORFX ORF1368 | Novel signal trans | Drosophila melanog | Human rab8 homolog | Human ovarian anti | Lung cancer associ | Amino acid sequenc | Human Rab10 protei | Human protein sequ |
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| | Query | Match | 100.0 | 98.8 | 75.3 | 49.5 | 49.3 | 48.9 | 48.1 | 48.0 | 48.0 | 48.0 |
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SM (HUMA-) HUMAN GENOME SCI INC Ruben Rosen CA, Barash SC,

WPI; 2001-465460/50. N-PSDB; AAS27053.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 701; 880pp; English

31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

Shimkets RA, Leach M; CURA-) CURAGEN CORP.

WPI; 2000-602362/57. N-PSDB; AAC75813.

31-MAR-2000; 2000WO-US08621

05-0CT-2000

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Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids can be used to express ORPX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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thrombosis; contraceptive

WO200058473-A2 Homo sapiens.

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2000US-0232397
2000US-0232398
2000US-0232400
2000US-0232401
2000US-0232401
2000US-0233063
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13-OCT-2000;
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20-OCT-2000;
  Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antilnflammatory; anti-HIV; antibacterial; antilnflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                      Novel signal transduction pathway protein, Seq ID 1120
                                                                                                                                                                                                                                                                                                                           2000US-0180628.
2000US-0184664.
2000US-0186350.
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2000US-0214886.
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              (first entry)
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11-MAR-2000;

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20-JUN-2000;

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08-SEP-2000;
08-SEP-2000;
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04-FEB-2000;
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02-MAR-2000;
             07-NOV-2001
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us-09-817-198a-2.rag

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 38802; 21pp + Sequence Listing; English.
                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 38802
                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
                                              (first entry)
                                                                                                                                                                                                                Drosophila melanogaster.
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N-PSDB; ABL14773.
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                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune (Isorders (e.g. congenital and acquired immunodeficiencies, autoimmune trasplant rejections and graft versus host disease, infectious diseases (e.g. transplant rejections and graft versus host disease, infectious diseases) (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood related disorders (slockle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal chormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. quincentlopephritis), cardiovascular disorders (e.g. daisorders (e.g. quincentlopephritis), cardiovascular disorders (e.g. daisorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17083 represent novel signal transduction contains an incomplex of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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Pred. No. 6.2e-80;
0; Mismatches 4;
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20000S-0251856
20000S-0251868
20000S-0251869
20000S-0251989
20000S-0254097
2000US-0259678
                                                               2000US-0251030.
2000US-0251988.
2000US-0256719.
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Best Local Similarity 97.6%;
Matches 160; Conservative
                        2000US-0250160.
2000US-0250391.
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Best Local Similarity
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N-PSDB; AAS27472.
                                                             05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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05-JAN-2001;
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Myers EW;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furges. The invention discloses genomic DNA sequences (ABLIGIT6-ABL30511), expressed DNA sequences (ABLIGIT6-ABL30511), expressed DNA
                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QIWDTAGOERFHTITTSYYRGAMGIMLVYDITNEKSFENIVKWLRNIDEHANEDVEKMIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%; Score 546.5; DB 22; Length 204; 49.8%; Pred. No. 1.4e-49; Live 47; Mismatches 50; Indels 9;
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Matches 105; Conservative
                                                                                                                                                                                                                                     (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                 204 AA;
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides. The polypeptides, methods of detecting the nucleotides of the invention. Although novel, many of the bolypeptides of the invention. Although novel, many of the polypeptides of the invention and though novel, many of the polypeptides of the invention have bomnology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; hammanomodulatory activity; tissue growth activity; chemotactic or chemokinetic activities; heemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be chromoditions, e.g., by protein or metastasis.

Conditions, e.g., by protein or gene therapy: such conditions include cancers, heemotopicit disorders (e.g., myeloid or lymphoid cell cancers, heemotopicit disorders (e.g., myeloid or lymphoid cell activities), arterial schaamatopicits, a therosclerosis, coronary heart disease.
                                                                                                               cytokine; cell proliferation; cell differentiation; growth factor; polesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to
                                                                                                                                                                                                        myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; chronic inflammatory condition; proliferative retinopathy; bone disorder; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                     haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                  Human rab8 homologue, SEQ ID NO:2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 276; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                      11-JAN-2002
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promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                      NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                 ö
                                                                                                                                                                             Length 213;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 43;
                                                                                                                                                                                  DB 22;
                                                                                                                                                                              49.3%; Score 545; DB 22; 52.9%; Pred. No. 2.1e-49; iive 45; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HCGMA67, SEQ ID NO:2465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP41333 standard; Protein; 221 AA.
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                                                                                                                                                                                                  Local Similarity 52.9 tes 99; Conservative
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                                                                                                                                                213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 RMRASNE 187
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                                                                                                                                                  Sequence
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                    Matches
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                                                                                      The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDMAs encoding them (ABQ54131-ABQ5305), and also encompasses polypeptides 90% identical and polyvucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens of ovarian antigens, antibodies against human ovarian antigens and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian canneer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system clastratic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, coplycystic ovary syndrome, ovarian cysts, and dymenorhoral, endocrine disorders, infertility, disorders of pregnancy, anovulation, coplycystic ovary syndrome, ovarian cysts, and dymenorhoral, endocrine disorders, infertions (e.g., chlamydia, HUV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anadiomain), cardiovascular disorders, autoimmune oophoritis, systemic lupus erythematosus, blood-related disorders. ouvarian antigen polypeptides and urinary system disorders. Ovarian antigen polypeptides and outland system disorders. Ovarian antigen polypeptides and curinary system disorders. Ovarian antigen polypeptides and curinary system disorders. Ovarian antigen properties may be used an formation of activity. The polypucleotides may be used as food additives or to prepare antibodies cuseful in disease diagnosis, drug targeting and aphenotyphing. The polymentic sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed certification, but was obtained and and and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 KADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQI 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer associated polypeptide sequence SEQ ID 534.
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                            Claim 11; SEQ ID No 2465; 2922pp; English.
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Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 AA;
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polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprofective; cytostatic; cardioactive; and antagonists may have neuroprofective; cytostatic; cardioactive; and antagonists may be used to the representable protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer associated colling cancer associated colling as the protein or polynucleotide sequences. The protein of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, chromosome associated associated alsoners. The protein protein may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18433 and peptide AAB58549 are used in the course of the invention for the course of the course of the invention for the course of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numerous other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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ilarity 47.6%; Pred. No. 6.2e-48;
Conservative 49; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1027-1028; 1425pp; English.
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                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
08-MAR-2000; 2000WO-US05918.
                                                                                             99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587514/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as lung cancer
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                                                                                             12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB19165;
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coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence represents the human Rablo protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                       a novel human Rabl0 cDNA sequence. The protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QIWDTAGQERFHIITSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                 Preparation of human gene coding sequence, its encoded polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.0%; Score 530.5; DB 21;
llarity 55.8%; Pred. No. 6.6e-48;
Conservative 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein sequence SEQ ID NO:17619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB95340 standard; Protein; 200 AA.
                                                                                                                                                                                                                                                                                                                    Claim 2; Page 18; 23pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                        98CN-0121911
                                                                                                            98CN-0121911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 96; Conservat
                                                                                                                                                                                      Gao J;
                                                                                                                                                                                                                          2000-400723/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AA;
                                                                                                                                                                                                                                             N-PSDB; AAA40104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
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                                                                                                                                               (UYFU-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                      Tu Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2000;
                                                                                                            28-SEP-1998;
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                                                                        28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001
CN1249345-A.
                                   05-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a mammalian RAB protein. RAB proteins constitute the largest family of small GTPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression .The DNA may also be used to identify expression of the gene in a biological specimen.
                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 QIWDTAGGERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                    Buckler AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying homologous or related genes, in producing compormodulates expression or function of RAB for cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                       RAB protein; GTPase; GTP binding; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                      Rutter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.0%; Score 530.5; DB 21;
55.8%; Pred. No. 6.6e-48;
tive 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                      Vega R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB09979 standard; Protein; 200 AA
 Amino acid sequence of human RAB10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 39; 58pp; English.
                                                                                                                                                                                                                                                                                                      B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Rab10; Yap/Rab family
                                                                                                                                                                                        13-MAR-2000; 2000WO-US06330.
                                                                                                                                                                                                                                                                                                        McIntosh
                                                                                                                                                                                                                             99US-0126083
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                                                                                                                                                                                                                                                                   (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
96; Conserva
                                                                                                                                                                                                                                                                                                                                           WPI; 2000-647233/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 AA;
                                                                                                                                                                                                                                                                                                      Abel K,
                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA96887
                                                                                                               WO200058464-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                              Homo sapiens
                                                                                                                                                                                                                             25-MAR-1999;
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                                                                                                                                                     05-OCT-2000
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                                                                                                                                                                                                                                                                                                        Allen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
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Best Loca Matches

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AAB0997

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Gaps

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WO200055174-A1.

21-SEP-2000,

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oilgo-dT primer and an oilgouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of an oilgonucleotide which comprises a 3'-end sequence of polynucleotide which comprises a 3'-end sequence, where the oilgonucleotide which comprises a 3'-end sequence, where the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the potential and of the full-length cDNAs. The primers are also useful for the full-length cDNAs as ally without any specialised methods. AAH13628 and AAH13633 to AAH13633 to AAH13632 to AAH13632 to AAH13632 to AAH13632 to a present human amino acid sequences; and AAH13632 to AAH13632 to a present human amino acid sequences; and AAH13632 to AAH13632 to a present oil sequences; and a better in the exemplification of the top control of the control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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     Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.0%; Score 530.5; DB 22; Length 200; 55.8%; Pred. No. 6.6e-48; Live 46; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate cancer antigen protein sequence SEQ ID NO:1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sogai T, Nishikawa T, Hayashi K, Saito K, Y
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                        Claim 8; SEQ ID 17619; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB56993 standard; Protein; 218 AA.
Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention
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Matches 96; Conserva
                                                                                  WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 AA;
                                                                                                                                                                                                                           full-length cDNAs
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                         Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                  proteins, called prostate cancer antigens, given in ABB5563 to AAB57302.

The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomedulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAR16506 to AAR16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                      AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.0%; Score 530.5; DB 21; Length 218; 55.8%; Pred. No. 7.5e-48; live 46; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                          Claim 11; Page 2014-2015; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #7257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG07266 standard; Protein; 218 AA.
                                                                                                                                                                                                                                                                                         disorders such as prostate cancer
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                            99US-0124270
                                                            08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                            Rosen CA, Ruben SM;
                                                                                                                                                                                                        WPI; 2000-587513/55.
N-PSDB; AAF16196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AA;
                                                                                                                                             ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2
                                                                                            .2-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                             (ROSE/)
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(PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                               N-PSDB; ABL15750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMEANN 181
pharmaceutical.
                                                                    WO200171042-A2
                                                                                                                                                                         23-MAR-2000;
                                                                                                                                                                                            11-JUL-2000;
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                                                                                                       27-SEP-2001
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Matches
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                                                                                                                                                                                                                                                                                                                                                                             polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapphing, and in recombinant production of (II). The and gene mapphing, and in recombinant production of (II). The and gene mapphing, and in recombinant production of (II). The conjunction of (II) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and porduce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to an an oaid sequences. ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-ABGOOLO-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 MAKKTYDLLFKLLLIGDSGVGKTCVLFRFSDDAFNTTFISTIGIDFKIKTVELQGKKIKL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.9%; Score 529.5; DB 22; Length
55.8%; Pred. No. 9.6e-48;
ive 46; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 41733.
                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 37625; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB71647 standard; Protein; 207 AA
                                                                                                                                                             Tang YT;
                                       30-MAR-2001; 2001WO-US08631
                                                                        2000US-0540217
2000US-0649167
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                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                 WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AA;
                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                 N-PSDB; AAS71453
                                                                          31-MAR-2000;
                                                                                            23-AUG-2000;
                                                                                                                                                                                                                                                                                                      biodiversity
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Matches 9
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ABB71647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 41733; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%; Score 528.5; DB 22;
53.8%; Pred. No. 1.1e-47;
iive 41; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human 27423 G-protein.
                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
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                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                              2000US-191637P
                                                                                                                                                                                                                                                                           2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 53.8
nes 100; Conservative
Drosophila melanogaster.
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The present sequence represents a human G-protein. The specification describes 3706, 2324, 27423, 32700 or 32712 small G-proteins. The G-protein polypeptides and polynucleotides are useful as a target for diagnosis and treatment of G-protein mediated or related disorders, and for identifying agonists and antagonists for diagnosis and treatment. They are useful for treating disorders of lung (e.g. congenital anomalies, pulmonary congestion, oedema, adult respiratory distress syndrome, haemorrhage, chronic obstructive pulmonary disease, asthma, Goodpasture's syndrome and pulmonary hypertension), liver (e.g. hepatic injury, jaundice, cholestasis, viral hepatitis, cirrhosis, Wilson's disease, autoimmune hepatitis and hepatic failure), and care meningencephalitis, allocated allocated intercental maningencephalitis, multiple sclerosis, amyotropic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                   hepatitis;
               chronic obstructive pulmonary disease; asthma; pulmonary hypertension; liver disorder; hepatic injury; jaundice; cholestasis, viral hepatitis cirrhosis; Wilson's disease; autoimmune hepatitis; hepatic failure; brain disorder; hypoxia; cerebral ischemia; intracranial haemorrhage; acute meningitis; parkinson's disease; Alzheimer's disease; glioma; chronic bacterial meningoencephalitis; multiple sclerosis; amyotropic lateral sclerosis; stroke; Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIKNWIRNIEEHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 INDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human small G-protein polypeptides and polynucleotides for treating lung disorders, liver disorders and brain disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.8%; Score 528.5; DB 22; Length 207;
adult respiratory distress syndrome; Goodpasture's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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47; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sclerosis, stroke and Huntington's disease).
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                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                               27-FEB-2001; 2001WO-US06292.
                                                                                                                                                                                                                                                                                                                    29-FEB-2000; 2000US-0185606.
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nes 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 AA;
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                                                                                                                                                                                                      WO200164887-A2.
                                                                                                                                                                                                                                            07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Meyers RA;
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The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide sequences defined in the specification, where the

coligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises at least 15 nucleotides and the combination of

the 5'-end sequence 3'-end sequence 15 selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

particularly full-length cDNAs. The primers are also useful for the

condection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

condection and an anino acid sequences; and AAH13638 and

AAH13633 to AAH18742 represent human amino acid sequences; and AAH13632

represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
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33;
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54.0%; Pred. No. 1.16
tive 47; Mismatches
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                                                                                                                                                                                                                                                           99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                           Homo sapiens
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11-JAN-2000;
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M38391 Discopyge o
BC000799 Homo sapi
X75593 H. sapiens m
AF48948 Homo sapi
M38390 Discopyge o
AF297660 Homo sapi
X56387 Canine rabi
X56387 Canine rabi
AF035646 Mus muscu
BC000896 Homo sapi
AF106681 Homo sapi
AF106681 Homo sapi
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X56385 Canine rab8
BC002977 Homo sapi
AK025165 Homo sapi
BC019990 Mus muscu
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AY042795 Arabidops
AY035132 Arabidops
AX236078 Sequence
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BC020654 Homo sapi
AX236076 Sequence
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M83679 Sprague-Daw
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BC013790 Mus muscu
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AY060425 Drosophil
AF498943 Homo sapi
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D84347 Drosophila
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     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1 MAKQYDVLFRLLLIGDSGVG.
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ALIGNMENTS

AK001111 Homo sapi AL833365 Homo sapi Z73948 L.japonicus AL136650 Homo sapi

AK001111 HSM804678

AX285080 Sequence AX285089 Sequence AX285091 Sequence

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TITLE
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        PAT 06-JUN-2002
                                                                                                                   Tang, Y.T., Asundi, V., Zhou, P., Xue, A.J., Ren, F., Zhang, J., Wang, J.R., Zhao, Q.A., Wang, D., Liu, C., Drmanac, R.T. and Wehrman, T. Wucletc acids and polypeptides
Patent: WO 0218424-A 74 07-MAR-2002;
HYSEQ, INC. (US)
                                                                                      Euteleostomi;
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Catarrhini; Hominidae; Homo.
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Mammalla; Eutheria; Primates;
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, K.W., Bouffard, G.C., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, K.W., Bouffard, G.C., Breen, K., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
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McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
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Mus musculus, clone MGC:38375 IMAGE:5345297, mRNA, complete cds.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 3139)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                       200
                                                                                                                                                                               680
180
                                                           620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissaue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NTSC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Rodentia;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
M83679.
LWW GTP-binding protein.
Rattus norvegicus (strain Sprague-Dawley) (library: LAMBDA ZAPII)
Rattus norvegicus
Rattus norvegicus
Rattus norvegicus
Rutus norvegicus
Rutus norvegicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1 (bases 1 to 945)
Elferink.L.A., Anzai,K. and Scheller,R.H.
rabl5, a novel low molecular weight GTP-binding
specifically expressed in rat brain
J. Biol. Chem. 267 (9), 5768-5775 (1992)
1313420
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Matches:
Conservative:
Mismatches:
Indels:
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1. .945
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220. .858
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                                                                                                                                                                                                              Mus musculus, clone MGC:6897 IMAGE:2655151, mRNA, complete cds. BC013790 BC013790.1 GI:15489393 MGC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg.R.

Direct Submission
Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: TRAK Plate: 5 Row: i Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MGC:6897 IMAGE:2655151"
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/clone_lib="NCL_CGAP_Mam2"
/lab_host="DH10B"
                                                                 WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Preparation: College of Medicine Human Genome
Sequencing Center
Genter Gode: BCM-HGS
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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INV 07-AUG-1997
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Submitted (01-AUG-1997) Koichi Ozaki, Osaka University, Graduate Submitted (01-AUG-1997) Koichi Ozaki, Osaka University, Graduate School of Science, Department of Biology: 1-1 Machikaneyama, Toyonaka, Osaka 560, Japan (E-mail:ozaki@bio.sci.osaka-u.ac.jp, Tel:+81-6-850-5439)
Location/Qualifiers
1.1613
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Satoh,A.K., Tokunaga,F. and Ozaki,K.
Rab proteins of Drosophila melanogaster: novel members of the Rab-protein family
FEBS Lett. 404 (1), 65-69 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (strain:Oregon R) head cDNA to mRNA.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
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     Length:
Matches:
Conservative:
Mismatches:
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/db_xref="taxon:7227"
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Rablo.
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100.00%
99.35%
72.22%
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Ozaki, K.
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Pterygota;

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Barkeley, CA 94720

Barkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection I (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracity this particular CDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptions that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to canadéfruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAL25464.1"
/db_xref="fu1:16648398"
/db_xref="fu1:16648398"
/db_xref="fu1:16648398"
/db_xref="purbase: Protein | 
                                                                                                                                                                                                                                        Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-OCT-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 9720, USA
Sequence submitted by:
                                                                                                                                                                                  Neoptéra; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
1 (bassa 1 to 2349)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson,
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/db_xref="FLYBASE:FBgn0015789"
255. .869
                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
     Drosophila melanogaster LD39986 full length cDNA.
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Lawrence Berkeley National Laboratory
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/db_xref="taxon:7227"
/map="19C1-19C1"
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/gene="Rab10"
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/tissue_type="head"
                                             /gene="DRab10"
257. 871
/gene="DRab10"
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546.50
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HSMRAB8
                                                                                                                       ORIGIN
                                                                                                                                                                  Score:
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                                                                                                                                                                                                                                                                                                                 Dβ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 bp mRNA linear PRI 01-MAY-200 small GTP binding protein RAB8 (RAB8) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outpublished

( bases 1 to 624)

Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S.

Direct Submission
Submitted (05-APR-2002) CDNA Resource Center, Guthrie Research
Institute, One Guthrie Square, Sayre, PA 18840, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                      AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                                                                                                                                                                                                   MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                                            GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
                                                                                                                                                                                                                                                                                   674
                                                                                                                                                                                                                                                                                                                  GluSerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGly 179
                                                                                                                                                                                                                                                                                                                                                                                           LeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLys 199
                                                                                                                                                                                                                                                                                                                                                                                                                -----AAGACATCAGGA 782
                                                                                      59
                                                                                                                                79
                                                                                                                                                                       80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle 99
GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                    ThrlleGlyValAspPheLysMetLysThrlleGluValAspGlyIleLysValArglle
                                                                                                                              GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                                                                                                                                                                                                                          1 (bases I to 624)
Puhl, H.L. III, Ikeda, S.R. and Aronstam, R.S.
Homo sapiens RAB family small GTP binding protein Unpublished
                                                                                                                                                                                                                                                                                                                                                               :::|||
| CGGGCCTTCTGCGAGCTGGCCGAGGCCATTCTGGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                     200 ProGluGlyProAlaAsnSerSerLysThrCys 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .624
/gene="RAB8"
1. .624
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AF498943.1
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REFERENCE
AUTHORS
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SOURCE
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AIRTIELDGKRIKLEGNECONDKRQVSKRENGEKLALDYGIKFMETSAKANINVEN
ARFTLARDIKAKNEGNEGSNGGYKITPDQQKRSSFFRCVLL"
147 c 165 9 124 t
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAGACCTGTGTCCGCTTCTCCGAGGACGCCTTCAACTCCACTTTAATCTCCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AACTGGATTCGCAACATTGAGGAGCACGCCTCTGCAGACGTCGAAAGATGATACTCGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AACAAGTGTGATGTGAATGACAAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleTrpAspThrAlaGlyGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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99
45
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Matches:
Conservative:
Mismatches:
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/gene="RAB8"
/note="RAB family member"
/codon_start=1
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545.00
77.018
52.948
49.328
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141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                             Aliqnment Scores:
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                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
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ORIGIN
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TITLE
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CFRAB8
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                                             Submitted (26-NOV-1990) A. Zahraoui, INSERM-U 248, 10 AVENUE DE VERDUN, 750-10 PARIS, FRANCE
2 (bases 1 to 660)
Zahraoui,A., Joberty,G., Arpin,M., Fontaine,J.J., Hellio,R.,
Tavitian,A. and Louvard,D.
A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells but colocalizes with the tight junction marker ZO-1
                                                                                                                                                                                                                                                                                                                     /product="rab8 small GTP binding protein"
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/db_xref="SWISS-PROT:P24407"
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AFFTLARDIKAKMMSKLEGNSFQGSNGCWKTPDQQKRSSFFRCVLL"
159 c 172 g 132 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
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/clone_lib="Human pheochromocytoma cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660
999
45
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                   in polarized epithelial cells
J. Cell Biol. 124 (1-2), 101-115 (1994)
8294494
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1-660)
                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                             /gene="rab8"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-817-198A-2 (1-212) x HSMRAB8
                                                                                                                                                                                                                                                                   /gene="rab8"
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545.00
77.018
52.948
49.328
                                     Direct Submission
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                      Zahraoui, A.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                           197
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So.:
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                                                 JOURNAL
                                                                                       AUTHORS
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           REFERENCE
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FRIRTIELDGKRIKLQIMDTAGQERFRTITTAXTRGAMGIMLYYDITNEKSFDNIRNW
FRIRTIEEHASADVEKMILGNKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVEN
AFFTLARDIKARMIKLEGNSPQGSNGVKITPDQQKRSSFFRCVLL"
190 c 196 g 159 t
                                                                                                                                                                                                 MAM 30-SEP-1999
                                                                                                                                                                                                                                                                            protein transport; ras gene; ras gene family
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-AUG-1990) Zerial M., EMBL, Meyerhofstrasse 1, 6900
Heidelberg, FRG
                                                                                                                                                                                                                                                                                                                                                                                        Chavier, P., Vingron, M., Sander, C., Simons, K. and Zerial, M. Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell line Mol. Cell. Biol. 10 (12), 6578-6585 (1990)
                  69
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SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu
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Canine rab8 mRNA for ras-related GTP-binding protein.
X56385
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999
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="GTP binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Canis familiaris"
/strain="cocker spaniel"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/protein_id="CAB56776.1"
/db_xref="G1:6006436"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_line="MDCK"
10. .633
                                                                             181 ArgMetArgAlaSerAsnGlu 187
                                                                                                                 551 AGCCCCCAGGGGAGCAACCAG 571
                                                                                                                                                                                                                                                    X56385.1 GI:920
GTP-binding protein; pi
Canis familiaris.
Canis familiaris
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10. .633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="rab8"
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545.00
77.018
52.948
49.328
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC002977 2048 bp mRNA linear PRI 12-JUL-2001
Homo sapiens, mel transforming oncogene (derived from cell line
NK14)- RAB8 homolog, clone MGC:2196 IMAGE:3547214, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Histo, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Scheth, Dunnes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission.
Submitted (06-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AACAAGIGIGAIGIGAACGACAAAAGACAAGIIIICCAAGGAACGGGGAGAAAAGCIGGCC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 CIGGACIAIGGAATCAAGTICAIGGAGACCAGIGCGAAGGCCAACAICAAIGGAGAAA 489
                                                                                        81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                               309
                                                                                                                                                                                                                                                                                                                       101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                        121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                                                                                                                                 310 AACTGGATTCGGAACATTGAGGAGCATGCTTCTGCAGATGTCGAAAAGATGATACTCGGA 369
                                                                09
                                                                                                                                                 80
                                                                                                                                                                                                                                                           61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                     IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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BC002977
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
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/translation="MaktyDylekilligdsgugktcvleresedafnstigid"
FKIRTIELDGKRIKLOIMDTAGGERETTTTAYYRAAMGIMLVYDTTNEKSFDNIRNW
IRNIEBHASADVEKMILGNKCDVNDKRQVSKERGEKLALDYGIKFMETSAKANINVEN
AFFTLARDIKAKMDNKKASSFRGNGGVKITPDQQKRSSFFRCVLL"
556 c 463 g 467 t
Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 8 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 452317.
                                                                                                                                                                                                                                                                                                                                            //...'vcdon_start=1
/product="mel transforming oncogene (derived from cell
line NK14)- RABB homolog"
/-----in id="AAH02977.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLysAlaAspGluGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 CTCGACTATGGAATCAAGTTCATGGAGACCAGCGCGAAGGCCCAACATGTGGGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 557 GCATTTTTCACTCTCGCCAGAGATATCAAAGCAAAAATGGACAAAAATTGGAAGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetalaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AAGACCTGTGTTCCGCTTCTCCGAGGACGCCTTCAACTCCACTTTTATCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                      /db_xref="LocusID:4218"
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/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2048
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAH02977.]
/db_xref="GI:12804237"
                                                                                                                                                                                                                                                                                                             /note="Vector: pOTB7"
                                                                                                               Location/Qualifiers
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52.948
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: angebon.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRKK Plate: 37 Row: c Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC019990 1337 bp mRNA linear ROD 07-AUG-2002 Mus musculus, Similar to mel transforming oncogene (derived from cell line NK14)- RABB homolog, clone MGC:28462 IMAGE:4161110, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                              121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                           81 AlaGlnGly1lePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                       101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                  546 AACTGGATTCGCAACATTGAGGAGCACGCCTCTGCAGACGTCGAAAAGATGATACTCGGG 605
                                                                                                                                                                                                                                                         141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                    161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                              426 ATATGGGACACAGCCGGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACAGGGGT 485
                                                                                         486 GCAATGGCCATCATGCTGGTCTACGACATCACCAACGAGAAGTCCTTCGACAACATCCGG
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/clone="MGC:28462 IMAGE:4161110"
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Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                    Kawabata,A, Hlkiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Skamatco,S., Okttani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Makamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDO human CDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert Sequencing: Research Association for Biotechnology; CDNA library construction, 5'- & 3'-and one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 ATGGCGAAGACCTACGATTACCTGTTCAAGCTGCTGATCGGGGGACTCGGGGGTGGGG 305
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Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL05769.
Homo sapiens
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AK025165
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/db_xref="taxon:9606"
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/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector ph
a 800 c 708 g 60
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                                                                                                                                                          2818 bp
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                     ArgMetArgAlaSerAsnGlu 187
                                                              617 AGCCCCCAGGGGAGCAACCAG 637
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ROD 07-AUG-2002

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GTP-binding protein.
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                                                                        /product="similar to mel transforming oncogene (derived from cell line NK14)- RAB8 homolog"
/protein_id="AAH1990.1"
/db_xref="cf:|48H1990.1"
/db_xref="cf:|48H1990.1"
/translation="MAKTYDYLFKLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGID FRIRILEDGRRIKLOJMPAGQERFRTTTAPXTRGAMGIMLYYDTINEKSFDNIRNW FRIRIEBHASADVEKMIGGNCDVNDKRQVSKERGEKLALDYGIKFMETSARANINVEN AFFTLARDIKANDKKLEGGNSPQGSSHGVKITVBQQKRTSFFRCSLL"
338 C 341 g 291 t
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Discopyge ommata GTP-binding protein (ora2) mRNA, complete cds.
M38391.1 GI:21311R
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Mismatches:
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Matches:
                                         /note="Vector: pCMV-SPORT6"
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                                                              /codon_start=1
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Best Local Similarity:
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/gene="ora2"
/codon_start=1
/product="GTP-binding protein"
/product="GTP-binding protein"
/protein_id="AAA4923.1"
/protein_id="AAA4923.1"
/protein_id="MAKTYDYDE
                         Discopyge ommata

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Marcinoidei; Marcinidae; Discopyge.

( bases 1 to 765)

Ngsee,J.K., Elferink,L.A. and Scheller,R.H.

A family of ras-like GTP-binding proteins expressed in electromotor
                                                                                                                                                                                                                                                                                                                                                        Unpublished (1990)
Draft entry and computer-readable sequence for [1] kindly submitted by J.K.Ngsee, 10-SEP-1990.
Dept of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] kindly submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 AAAACCTGCCTCTTCCGCTTCTCGGAGGACGCCTTCAACACCACCTTCATCTCCACC 133
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ommata electric lobe electromotor neuron, cDNA to mRNA.
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:7785"
/cell_type="electromotor neuron"
/tissue_type="electric lobe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanford University
Stanford, CA 94305-5020

Draft entry and computer-readable
by J.K. Ngsee, 10-SEP-1990.

Dept of Biological Sciences
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Stanford, CA 94305-5020.
Location/Qualifiers
1. .765
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14. .646
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FKIRTYDIEGKKIKLQVWDPAGQERFKTITTAYYRCAMGIILVYDTTDEKSFENIQNW
MKSIKENASAGVERLLLGNKCDMEAKRKVQKEQADKLAREHGIRFFETSAKSSMNVDE
ASSSLAMBDILLKSGGRRSGGRRSGRNFNKCSLG"
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  /product="RAB13, member RAS oncogene family"
/protein_id="AAH00799.1"
/db_xref="GI:12654003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 9438
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC000799 1211 bp mRNA linear PRI 12-JUL-:
Homo sapiens, RAB13, member RAS oncogene family, clone MGC:5074
101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                      AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                     LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                    434 ATAGATTATGGGATAAAGTTCCTGGAAACCAGCGCAAAATCCAGCATAAACGTTGAAGAG 493
                                                                                                                                                                                                                                              SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                                                                                                                          181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGlu---LeuGluGluGluGluGlyLys 199
                                                                                                                                                                                                                                                                                                                                                   494 GCATTTATTACACTTGCACGAGATATCATGACGAAACTCAACAAGAAAATG-----
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/tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
95. 706
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE:3451945, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                590 CCAAAGAACCCAGTCAAAAAAAG
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MGC.
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TITLE
JOURNAL
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BC000799
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1 (bases 1 to 1238)

2 abraoul, A., Joberty, G., Arpin, M., Fontaine, J.J., Hellio, R.,
Tavitian, A. and Louvard, D.
A small rab GTPase is distributed in cytoplasmic vesicles in non
polarized cells but colocalizes with the tight junction marker 20-1
in polarized epithelial cells
J. Cell Biol. 124 (1-2), 101-115 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:P51153"
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MKSIKENASAGVELLGKNCDMBARRYQREQADKLAREHGIRFFETSAKSSMNVDE
AFSSLARDILLKSGGRRSGNGNKPPSTDLKTCDKKNTNKCSLG"

275 c 355 g 244 t
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                              ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 40
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                                                                                                                                                                                                                                                                      2 (bases 1 to 1238)
Zahraoui,A.
Direct Submission
Submitted (03-NOV-1993) A. Zahraoui, INSERM U.248, 10 Avenue verdun, 75010 Paris, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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43.40%
                 X75593.1 GI:452319
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Homo sapiens
                                    rab13 gene.
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Best Local Similarity:
Query Match:
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619
                                                                                                          141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                                                                                                      -----GlnAlaHisArgLysGlu 176
                                                                                                                                                                                                                                                                                                LeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGlu 196
                                                                                                                                                                                                                                                                                                                              739 CICCCIGGGCIGAGGACCCITICTIGCCICCCCACCCCGGAAGCIGAACCIGAGGGAGAC 798
                                                                                                                           :::|||::: ||||
620 GCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGGAAAC
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                                                                                                                                                                                                                                                                 680 GCCAACAAGCCTCCCAGTACTGACCTGAAACTTGTGACAAGAAGAA-CACCAACAAGTG
                                                                                                                                                                                                                                                                                                                                                         197 GluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrp 211
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Search completed: November 17, 2002, 21:32:05 Job time: 2670 secs

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November 17, 2002, 18:07:04; Search time 67 Seconds (without alignments) 421.629 Million cell updates/sec
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GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 22 ABG07266 22 ABG07266 22 ABG71647 22 AAG67154 22 AAB92628 21 AAB99982 | AAG0998 AAG0968 AAG5394 AAG5394 AAG0868 AAG3521 | AAG0800 ABG0800 AAG4782 AAG4782 AAG2336 AAY0091 AAU2802 | | ABB5980 AAG3071 AAG3070 AAG4532 AAB1916 AAM3960 |
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| | 447.0 477.0 477.0 46.5 46.5 | 444444444 90000000000000000000000000000 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | |
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ALIGNMENTS

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RESULT 1
AAU17136
ID AAU17136;

XX
AC AAU17136;

XX
DE Novel signal transduction pathway protein, Seq ID 701.

XX
N Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;

XW
N Neuroprotective; cytostatic; dermatological; inflammatory; cancer;

IMM antiinflammatory; anti-HIV; antibacterial; antiinflammatory condition;

XW
N Neuroprotective; cytostatic; dermatological; inflammatory condition;

XW
N organ transplant rejection; infection; hepatitis C; blood disorder;

XM
N organ transplant rejection; infection; hepatitis C; blood disorder;

XM
N organ transplant rejection; infection; disorder; disorder;

XM
N organ transplant rejection; infection; disorder; disorder;

XM
N organ transplant respiratory; wound healing; endocrine; Adison's disease;

XM
N ocquired immune deficiency syndrome.

XM
N woloo154733-A1.

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N WO200154733-A1.

XM
N WAR-2000; 2000US-0119065.

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N 1-JAN-2000; 2000US-0118628.

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N A-FEB-2000; 2000US-0118628.

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116 - MAR - 2000; 20 11 - MAR - 2000; 20 - 4 MAG - 
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13 - OCT - 2000)
20 - OCT 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 10-DEC-2000; 05-DEC-2000; 06-DEC-2000; 17 - NOV - 2000; 17 - NOV - 2000; 17 - NOV - 2000; 05-JAN-2001;

SM Ruben (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-465460/50. N-PSDB; AAS27053.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders

Claim 1; SEQ ID No 701; 880pp; English

us-09-817-198a-2.rag

05-0CT-2000.

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The invention relates to novel isolated polypeptides (I), and display to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune clasorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant relactions and graft versus host diseases, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. quomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. datorder (inflammatory disorders), liver disorders (circhosis), as stimulators of B-cell responsiveness to pathogens, activators of tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (Albs). AAU17069-AAU17083 represent novel signal transduction cycles pathway protein, amino acid sequences of the invention.
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ö Gaps ; Indels Query Match 100.0%; Score 1105; DB 22; Best Local Similarity 100.0%; Pred. No. 2.1e-108; Matches 212; Conservative 0; Mismatches 0;

86 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60 -1 27 g 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120 δ

87

NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180 121 147 g ö

RMRASNELALAELEEEGKPEGPANSSKTCWC 212 181 οy

207 q

RESULT 2 AAB41604

AAB41604 standard; Protein; 218 AA

AAB41604;

(first entry) 08-FEB-2001 Human ORFX ORF1368 polypeptide sequence SEQ ID NO:2736.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; coaqulation; thrombosis; contraceptive.

WO200058473-A2 Homo sapiens.

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; capulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; on preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the proteins and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, cythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic aneamia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinifiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1979-1980; 5507pp; English.
                                                                                                           99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                          05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                          Shimkets RA, Leach M;
                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
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Gaps 9 Ouery Match 98.8%; Score 1092; DB 21; Length 218; Best Local Similarity 97.2%; Pred. No. 2e-107; Matches 212; Conservative 0; Mismatches 0; Indels 6

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IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120 9 ò 셤

61

ŏ Db δy a

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AAU17555 standard; Protein; 188 RESULT 3 SX E

AAU17555;

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15 - SEP - 2000;

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25 - SEP - 2000;

26 - SEP - 2000;

27 - SEP - 2000;

28 - SEP - 2000;

29 - SEP - 2000;

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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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   Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality; bown syndrome; ischaemia; renal disorder; cardiovascular; respiratory; bown syndrome; ischaemia; renal disorder; reproductive system; gastrointestinal; liver disorder; Aldison's disease; acquired immune deficiency syndrome.
                                  Novel signal transduction pathway protein, Seg ID 1120.
                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01312
           07-NOV-2001 (first entry)
                                                                                                                                                                                                                    WO200154733-A1
                                                                                                                                                                                                Homo sapiens
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ABB70670;
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ABB11916
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                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel isolated polypeptides (I), and purelectides (II). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, hemoglobin abnormalities and other blood-related disorders (else cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal disorders (e.g. glown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomenulomephritis), candiovascular disorders (e.g. glomenulomephritis), candiovascular disorders (e.g. disease), respiratory disorders, dermarclogical disorders (e.g. disease), reproductive system disorders (e.g. disease), reproductive system disorders (e.g. disorders (e.g. disorders), liver disorders, gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AA017059-AA017683 represent novel signal transduction pathway protein, amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                      Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NKADEEQXRQVGREQGQXLAXEYGMDFYETSACTNLNIKESFTR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 832; DB 22;
Pred. No. 6.2e-80;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 1120; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB70670 standard; Protein; 204 AA.
                                                                                                                                                                                                                                      Ruben SM;
            2000US-0250160.
2000US-0250391.
2000US-0251030.
                                                   2000US-0251988.
2000US-0256719.
2000US-0251479.
                                                                                          20000S-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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97.6%;
                                                                                                                                                  2000US-0251990.
2000US-0254097.
                                                                                                                                                                               2001US-0259678
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                                                                                                                                                                                                                                                             2001-465460/50
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Best Local Similarity
                                                                                                                                                                                                                                                                             N-PSDB; AAS27472
                                      05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
                                                                                                                                                                               05-JAN-2001;
                                                                                            08-DEC-2000;
                                                                                                           08-DEC-2000;
                                                                                                                       08-DEC-2000;
                                                                                                                                                                                                                                    Rosen CA,
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ID ABB7
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(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITG-ABL30511), expressed DNA sequences (ABLIGITG-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.5%; Score 546.5; DB 22; Length 204; 49.8%; Pred. No. 1.4e-49; Ive 47; Mismatches 50; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 38802; 21pp + Sequence Listing; English.
                                                          Drosophila melanogaster polypeptide SEQ ID NO 38802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 LRMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
   (first entry)
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Matches 105; Conservative
                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /enter JC, Adams M,
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N-PSDB; ABL14773.
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                                                                                                                                                                                                                                                                 WO200171042-A2.
                                                                                                                                                pharmaceutical
26-MAR-2002
                                                                                                                                                                                                                                                                                                                            27-SEP-2001.
                                                                                                                    Drosophila;
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB00825-ABA09574 represent nucleic acids encoding them. The Invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

CC antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of detecting the nucleotides or polypeptides of the invention. Although novel, many of the polypeptides of the invention have bomology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth activity; have various activities; stem cell growth activity; have various activities; activities; nemeostatic, thrombotic or chemokinetic activities; haemostatic, thrombotic or thrombotic or chemokinetic activities; phemostatic or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC chemotogram are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haemotopoletic disorders (e.g., myeloid or lymphoid cell cancers, haemotopoletic disorders (e.g., myeloid or lymphoid call seaso, are the invention are useful for preventing, the invent disease, are useful for preventing them may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound hamunomodulatory activities may be used in the immunomodulatory activities may be used in the immunomodulatory activity may be used in the immunomodulatory activit
                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                                                                                                   haematopoiesis regulation, tissue growth, immunomodulator; activin, inhibin, chemotaxis, chemokinesis, thrombolyyais, oncogenesis, proliferation, metastasis, cancer; tumour; haematopoietic disorder; proliferation; metastasis, cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; arthritis, chronic inflammatory condition; proliferative retinopathy; bone disorder; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammallan subject e.g. arthritis and cancer -
                                                                           Human rab8 homologue, SEQ ID NO:2286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C, Drmanac RT;
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27-APR-2000; 2000US-0560875.
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                          (first entry)
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nucleotides
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promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotid may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   67 IWDTAGQERFRIITTAYYRGAMGIMLVYDIINEKSFDNIRNWIRNIEEHASADVEKMILG 126
                                                                                                                                                                                                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                              NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                  7 MAKTYDYLFKLLLIGDSGVGKTCVLFRFSEDAFNSTFISTIGIDFKIRTIELDGKRIKLQ
                                                                                                                                                                                                                             ;
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                                                                                                                                                                                         Length 213;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                             43;
                                                                                                                                                                                         49.3%; Score 545; DB 22; 52.9%; Pred. No. 2.1e-49; iive 45; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian antigen HCGMA67, SEQ ID NO:2465.
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                                                                                                                                                                                       Query Match
Best Local Similarity 52.98
Matches 99; Conservative
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                                                                                                                                                        213 AA;
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                                                                                                                                                        Sequence
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neurological diseases

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Query Match
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                                                                                                                                                                                            recombinant vectors and host cells compitising numan ovarian antigen polynucleotides against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, colycystic ovary syndrome, ovarian cysts, and dymenorinoea), endocrine disorders, infertility, disorders of pregnancy, anovulation, colycystic ovary syndrome, ovarian cysts, and dymenorinoea), endocrine disorders, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anogenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), crespiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and colynucleotides may also be used in screening for compounds which colynucleotides may be used as food additives or to prepare antibodies cuseful in disease diagnosis, drug targeting and aphenotyphing. The printed cuseful in disease datagnosis, drug targeting and aphenotyphing. The printed sequence data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from WIPO at the colon of the colon of the printed constitution of the printed colon of the colon of the printed colon of the printed colon of the colon of the printed colon of the patent did not form part of the printed colon of the printed colon of the patent did not form part of the printed colon of the colon of the
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                                                                    The invention relates to 2175 novel human ovarian antigens (ABP41054-8P4912328) and to cDNAs encoding them (ABD54131-ABD56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 WDTAGQERFRIITTAYYRGAMGIMLVYDIINEKSFDNIRNMIRNIEEHASADVEKMILGN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 KADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.9%; Score 540; DB 23; Length 221; 52.7%; Pred. No. 7.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung cancer associated polypeptide sequence SEQ ID 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Mismatches
                   Claim 11; SEQ ID No 2465; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB58196 standard; Protein; 246 AA.
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Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 MRASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : II:
196 PQGSNQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB58196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB58196
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numerous other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonists may have neuroprotective; cytostatic; cardioactive; immunomodilatory; mustonitestinal immunomodilatory; mustonites general; violntestinal general; nephrotropic; antinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds an infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 MAKAYDHLFKLLLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKKKLQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.1%; Score 532; DB 21;
47.6%; Pred. No. 6.2e-48;
iive 49; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1027-1028; 1425pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 GRRSGN-----GNKP--PSTDLKTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19165 standard; Protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
(ROSE/) ROSEN C A.
                                                                                                                                     08-MAR-2000; 2000WO-US05918.
                                                                                                                                                                                                          99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-587514/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF18072
WO200055180-A2.
                                                                                                                                                                                                          12-MAR-1999;
                                                                    21-SEP-2000
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Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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This invention describes a novel human Rablo cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rablo. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence represents the human Rablo protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QIMDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERWLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                Preparation of human gene coding sequence, its encoded polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 530.5; DB 21;
ilarity 55.8%; Pred. No. 6.6e-48;
Conservative 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence SEQ ID NO:17619.
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                                                                                                                                                                                                                                                                                                                   Claim 2; Page 18; 23pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95340 standard; Protein; 200
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                       98CN-0121911
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                                                                                                                                                                                     Gao J;
                                                                                                                                                                                                                      2000-400723/35
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es 96; Conserv
                                                                                                                                                 FUDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AA;
                                                                                                                                                                                                                                          N-PSDB; AAA40104
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27-AUG-1999;
11-JAN-2000;
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09-JUN-2000;
                                                                                                                                                 (UYFU-) UNIV
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                                                                                                          28-SEP-1998;
                                                                                                                                                                                     Tu Q,
                                                                       28-SEP-1998;
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CN1249345-A.
                                  05-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a mammalian RAB protein. RAB proteins constitute the largest family of small GTPases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modilate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiclogical pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression .The DNA may also be used to identify expression of the gene in a biological specimen.
                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding a mammalian RAB protein useful for identifying homologous or related genes, in producing composition that modulates expression or function of RAB for cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                Buckler AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 530.5; DB 21; Lenycus
55.8%; Pred. No. 6.6e-48;
Virmatrhes 29; Indels
                                  RAB protein; GTPase; GTP binding; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                Rutter M,
                                                                                                                                                                                                                                                                                                  Vega R,
Amino acid sequence of human RAB10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB09979 standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 39; 58pp; English.
                                                                                                                                                                                                                                                                                                McIntosh B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Rablo; Yap/Rab family
                                                                                                                                                                                   13-MAR-2000; 2000WO-US06330
                                                                                                                                                                                                                        99US-0126083
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                                                                                                                                                                                                                                                             (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647233/62.
N-PSDB; AAA96887.
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                                                                                                                                                                                                                                                                                                Abel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 AA;
                                                                                                          WO200058464-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-2000
                                                                                                                                                                                                                        25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                       Homo sapiens
                                                                                                                                               05-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                              Allen M,
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Query Match Best Loca Matches

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Gaps

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Indels

DB 21; Length 200;

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The present invention describes primer sets for synthesising 5602

[10] Length cDNAs defined in the specification. Where a primer set

[11] Comprises: (a) an oligo-dT primer and an oligonucleotide complementary

[12] Complementary strand of a polynucleotide which comprises one of

[13] Complementary strand of a polynucleotides, or (b) a combination

[13] Complementary strand of a polynucleotides; or (b) a combination

[13] Complementary strand of a polynucleotide which comprises a 5'-end

[14] Sequence and an oligonucleotide comprising a sequence complementary to the

[15] Sequence and an oligonucleotide comprising a sequence complementary to a

[16] polynucleotide which comprises at 3'-end sequence, where the

[17] Sequence of an oligonucleotide comprises as 1'-end sequence, where the

[18] Sequence of an oligonucleotide sequence, where the

[18] Sequence of a polynucleotide sequence, and a polynucleotides,

[18] Sequence of a polynucleotides and beliance of the abortal sequences, and AHI3628 and

[18] Sequence of a polynucleotide sequences, and AHI3629 to AHH3632

[18] Septement human anino acid sequences; and AHI3632

[18] Septement human anino acid sequences; and AHI3632

[18] Septement human anino acid sequences; and AHI3632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILLI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNGKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
     Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer antigen protein sequence SEQ ID NO:1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
  Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.0%; Score 530.5; DB 22; 55.8%; Pred. No. 6.6e-48; Live 46; Mismatches 29;
                                                                                                                                                                                                                                           Claim 8; SEQ ID 17619; 2537pp + CD ROM; English.
sogai T, Nishikawa T, Hayashi K, Si
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB56993 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention
                                                                       WPI; 2001-318749/34
                                                                                                                                                                                               full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AA;
  Isoqai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB56993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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proteins, called prostate cancer antigens, given in ABB5333 to ABB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, valnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAR16506 to AAR16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 MAKKTYDLLFKLLIGDSGVGKTCVLFRFSDDAFNTFISTIGIDFKIKTVELQGKKIKL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                      AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.0%; Score 530.5; DB 21; Length 218; 55.8%; Pred. No. 7.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Mismatches
                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 2014-2015; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #7257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG07266 standard; Protein; 218 AA.
                                                                                                                                                                                                                                                                                                                  disorders such as prostate cancer
                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
(ROSE/) ROSEN C A.
                                                                   08-MAR-2000; 2000WO-US05988
                                                                                                   99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                            Rosen CA, Ruben SM;
                                                                                                                                                                                                                         WPI; 2000-587513/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AA;
                                                                                                                                                                                                                                             N-PSDB; AAF16196
WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                     12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                  21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                     23-MAR-2001; 2001WO-US09231.
                          Drosophila melanogaster.
                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                    (PEKE ) PE CORP NY
                                                                                                                                                                                                                                   N-PSDB; ABL15750
pharmaceutical.
                                                   WO200171042-A2
                                                                                                                                                                                                                                                                                   interactions
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                                                                           27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disconders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human conduction, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>.</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.9%; Score 529.5; DB 22; Length 55.8%; Pred. No. 9.6e-48; Live 46; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 41733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 37625; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB71647 standard; Protein; 207 AA
                                                                                                                     Tang YT;
                             30-MAR-2001; 2001WO-US08631.
                                                    2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                              WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AA;
                                                                                             HYSE-) HYSEQ INC
                                                                                                                                                           N-PSDB; AAS71453
                                                     31-MAR-2000;
                                                                   23-AUG-2000;
                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
    11-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITQEKSFENIKNWIRNIEENASADVEKMLLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NKADBEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 207;
                                                                                                                             Disclosure; SEQ ID NO 41733; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%; Score 528.5; DB :
ilarity 53.8%; Pred. No. 1.1e-47.
Conservative 41; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of human 27423 G-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG67154 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA;
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RMEANN 181
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The present sequence represents a human G-protein. The specification describes 37705, 23224, 27423, 37700 or 32712 small G-proteins. The G-protein polypeptides and polynucleotides are useful as a target for diagnosis and treatment of G-protein mediated or related disorders, and for identifying agonists and antagonists for diagnosis and treatment. They are useful for treating disorders of lung (e.g. congenital anomalies, pulmonary congestion, oedema, adult respiratory distress syndrome, haemorrhage, chronic obstructive pulmonary disease, asthma, Goodpasture's syndrome and pulmonary hypertension), liver (e.g. hepatic injury, jaundice, cholestasis, viral hepatitis, cirrhosis, wilson's disease, autoimune hepatitis and hepatic failure), and brain (e.g. hypoxia, cerebral ischemia, intracranial haemorrhage, acute meningitis, Parkinson's disease, Alzheimer's disease, gliomas, chronic bacterial meningencephalitis, multiple sclerosis, amyotropic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
             chronic obstructive pulmonary disease; asthma; pulmonary hypertension; liver disorder; hepatic injury; jaundice; cholestasis; viral hepatitis; cirrhosis; Wilson's disease; autoimmune hepatitis; hepatic failure; brain disorder; hypoxia; cerebral ischemia; intracranial haemorrhage; acute meningitis; Parkinson's disease; Alzheimer's disease; glioma; chronic bacterial meningoencephalitis; multiple sclerosis; amyotropic lateral sclerosis; stroke; Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human small G-protein polypeptides and polynucleotides for treating lung disorders, liver disorders and brain disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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respiratory distress syndrome; Goodpasture's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.8%; Score 528.5;
54.0%; Pred. No. 1.1e
tive 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB92628 standard; Protein; 207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 15; 151pp; English.
                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                 27-FEB-2001; 2001WO-US06292.
                                                                                                                                                                                                                                                                                                       29-FEB-2000; 2000US-0185606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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tes 95; Conserv
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                                                                                                                                                                                            WO200164887-A2.
                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                  07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                               Meyers RA;
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The present invention describes primer sets for synthesising 5602

(inll-length cDNAs defined in the specification. Where a primer set

comprises: (a) an oligo-dT primer and an oligonucleotide complementary

to the complementary strand of a polynucleotide which comprises one of

the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination

oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises at 3'-end sequence, where the

oligonucleotide which comprises at selected from those defined in

the specification. The primer sets can be used in antisense therapy and

in gene therapy. The primer sets can be used in antisense therapy and

on gene therapy. The primers are useful for synthesising polynucleotides,

particularly full-length cONAs. The primers are also useful for the

connected and primers are useful for synthesising polynucleotides,

particularly full-length cONAs. The primers are also useful for the

connected and primers are useful for synthesising polynucleotides,

particularly full-length cONAs. The primers are also useful for the

connected and any specialised methods. AAH13628 and

AAH13633 to AAH13642 represent human amino acid sequences; and AAH13632

represent cliquourleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIKNWIRNIEEHASSDVERMILG 120
                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                      sogai T, Nishikawa T, Hayashi K, Saito K, Y.
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 10930; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%; Score 528.5; DB 2.54.0%; Pred. No. 1.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                  Human protein sequence SEQ ID NO:10930.
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2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                        28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                99JP-0248036
                                                                                                                                                                                                                                                                                                                          2000JP-0241899
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es 95; Conserv
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                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                            Homo sapiens
                                                                                                                              EP1074617-A2
                                                                                                                                                                                                                                                                                                                            09-JUN-2000;
                                                                                                                                                                                                                                                29-JUL-1999;
                                                                                                                                                                    07-FEB-2001.
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`` Search completed: November 17, 2002, 20:38:26
Job time : 68 secs

Sequence 44, Appli Sequence 1, Appli Sequence 15, Appli Sequence 15, Appli Sequence 1703, Appli Sequence 1703, Appli Sequence 1703, Appli Sequence 235, Appli Sequence 235, Appli Sequence 2113, Appli Sequence 2113, Appli Sequence 374, Appli Sequence 374, Appli Sequence 374, Appli Sequence 774, Appli Sequence 774, Appli

Sequence 6

Sequence 1461, Ap Sequence 10, Appl Sequence 13, Appl Sequence 33, Appl Sequence 49, Appl

Sequence 1359, Sequence 33, A

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Sequence 1, Application US/09817198A
Patent No. US20020146758A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTA 180
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                                   0 US-09-967-736-4

US-09-944-531-1359

US-09-917-198A-33

US-09-919-172-49

US-09-919-172-49

US-09-919-172-49

US-09-919-172-49

US-09-919-172-49

US-09-919-170-445-478

US-09-770-445-478

US-09-770-445-478

US-09-917-182-1

US-09-918-945-4

US-09-938-842A-2113

US-09-938-842A-2113

US-09-938-842A-2113

US-09-938-842A-313

US-09-938-842A-314

US-09-938-842A-314

US-09-938-842A-314

US-09-938-842A-774

US-09-938-842A-774

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US-09-770-445-469

US-09-770-445-469
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Matches 3257; Conserv
    ORGANISM: Human
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LENGTH: 3257
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US-09-817-198A-1
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| 241 GGCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTT | 301 IGGTCTATGACATTAGCAGCGCACCTCTTACCAGCACATCATGAAGTGGGTCAGTGACG | 361 IGGATGAGTACGCACCAGAAGCGTCCAGAAGATCCTTATTGGAATAAGGCTGATGAGG | 421 AGCAGAAACGGCAGGTGGGAAGAGAACAAGGCAGCAGCTGGCGAAGGAGTATGGCATGG | 481 ACTICIAIGAAACAAGIGCCIGCACCAACCICAACATIAAAGAGICATICACGCGICIGA | 541 CAGAGCTGGTGCTGCAGGCCCATAGGAAGGAGCGTGGAAGGCCTCCGGATGCGTGCCAGCA | 601 ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGCCAAACCCGAGGGCCCAGCGAACT | 661 CTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCACACGACACCACCTCTTCC | 721 CTCAGGAGGCCCGTGGGCAGCAGGGAGCCGGGGCTTTGCCCTGCTGCTGCTCTCTCGT | 781 GTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCTGCCTG | 841 CTGCTGTCATCTCAAGCAGCCCTGTCCCCAGCCGTCCACCCTGGAGTGGTCTTCTTCA | 901 GCCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCAGGATGTGCCGCAAGCACTGTCTC | 961 ACCATCCCGCACCACCAGACAACAGCCAGGGCTGGAGTCCAGGCCACTTTCAGCTGCTC | 1021 CTTTCTCCGTGCATCGTGTCTCTTCTCTGCTTTTCTCTCTTTCCCCCACTTCTCTTTCTCTTCTCTTCT | 1081 TGACCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCGGTCCCCGTGTGT | 1141 CCTGCTGTGTGCAGCTCGCTCTTTCCTTCCTTCCTAGCTATCCAAGGGGATGGACCCAG | 1201 GCTCGTGGGGAGGTTCCACCCTTGGATCCAGGAAGACCCTCCACCCTGCCTCGTGGGTG [| 1261 GGCCAAAGGCTACAGGGTGCTTCTTCCTCCCCACCCCCACTGTCCCTGTGCCACTGTCCCTGTGTGCCACTGTCCTGTGTGCCACTGTCCCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCACCCCACCCA | 1321 TGGCCTGCCTCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGAAACAGCAA |
| q | oy Dp | çy Qa | Qy | Qy Dp | Oy Dp | Oy Dp | oy Op | Qy Dp | Qy Db | Qy | QY | QY | Qy | Qy | Qy Db | Oy Dp | Oy Db | oy da |

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| QΥ | 1381 | 4 | |
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| qq | 1381 | CGGGGAGTCCTCGAGCCTGGGGCTGCCTACCTCTACCCCATTCCCCGACCAGGCTTTG | |
| QY | 1441 | 0 | |
| qq | 1441 | CCTIGCTIGGCIGCCCGCCTGCTTIGGGGAACTGAGCTCAGAGGCAGGTGCTTCA | |
| Qy | 1501 | GAAGGAAACAAAATGAGGGGGGGGGGAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCA 156 | |
| qq | 1501 | aaggaaacaaaatgaggggrggcaggaraaaaagrcacccartcrcaaccccca 156 | |
| QY | 1561 | TTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGC 16 | |
| qa | 1561 | GCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGC 162 | |
| Qy | 1621 | 8 | |
| QQ | 1621 | TGTGGGTACTCCAGGGGCAAGGAGCCCTGGGGTCAGTGACACTGTCAGGCCAACCAT 168 | |
| QY | 1681 | GCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGGTCCTATGTATCAGGTTAAGA 1740 | |
| qq | 1681 | CACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCAGGTTAAGA 174 | |
| Qy | 1741 | 0 | |
| qa | 1741 | CAAGGGAGAGTTGGCCAGGGACAGCAGTTTGCACAGCAGAGGGGAATGTAGCAACAGCA 180 | |
| QY | 1801 | GGGCCTCCTAGGCCCCATCTTCCATAGGAAGAAGACATTCCTCAGACTCCCA 1860 | |
| qq | 1801 | GGCCTCCTAGGCCCCCATCTTCTTTCTTAGGTAAGAAGAGCATTTCCTCAGACTCCCA 186 | _ |
| QY | 1861 | AGGACTGAGCCTAGCCTTCAGCAACGATCTCCTGGGACCCAAAGTTTATGG 19 | _ |
| QQ | 1861 | GCGGAGGACTGAGCCTACAGCAACCAAGGTTCTCCTGGGACCCAAAGTTTATGG 192 | _ |
| QY | 1921 | GGGTAGAAACGCTTGGTG 198 | _ |
| QO | 1921 | AGAAGGGCAAAGACTTCATGGGAAGAGGAAGGAAGGCCCTGGGTAGAAACGCTTGGTG 198 | _ |
| Qy | 1981 | TIGCCCTITAAGACAAAGCGCTCATCTIGCCCTCTACCTCCTGAIAGGCTT 204 | _ |
| QQ | 1981 | TGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGCCCTCTACCTCCTGATAGGCTT 204 | _ |
| QY | 2041 | CCAACCACACTGTGGCTACAGGTGGAGGGAAGAGGACTCCTTCCT | _ |
| qq | 2041 | SGTTTGCCAACCACACTGTGGCTACAGGTGGAGGGAAGAGGACTCCTTCCT | _ |
| QY | 2101 | AGGAAGITICTITAACCCCATAIGGCCCAAGAGTAGCTCGTAGGAGGCCC | _ |
| qq | 2101 | GCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAGCTCGTAGGAGGCCC 21 | _ |
| QY | 2161 | 22 | _ |
| QQ | 2161 | TTAAAGACGGAACAAGTAATTTACCAGTTCTACTGGGGTTCCTGCCCACGTCCCAAG | _ |
| QY | 2221 | GTCATTC | _ |
| qa | 2221 | GGGCGAGGCCTAGGAAGAGGGTCATTCTTAAGCCACACATTAGCTGCACTGCGTGGCT | _ |
| QY | 2281 | CAGCCAAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAATCCAGGGCA 2340 | _ |
| QQ | 2281 | AGCCAAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAATCCAGGGCA 234 | _ |
| Qy | 2341 | TCTATATGTGAAGGATAAGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGA 240 | _ |
| qa | 2341 | CATAIGIGAAGGAIAAGAACCICACIICCIIACICCICCAAAAAGAAGIGGGGAAAGA 24 | _ |
| Qy | 2401 | 46 | _ |
| QQ | 2401 | CATCAAACCTTTCCTCCTGACTTACCAAACCAGGAAAACAGCAGGAGAGGGTGCTC | _ |

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Score 2696.6;
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Matches 2717; Conserv
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GGACTTAGGGACAGGGTATAGCTTAGATGGTGGAAAGCAAAGGAGGAGGAGGTTGTAA
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ENCODING
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TILE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEII;
TILLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODII;
TILLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODII;
TILLE PREPRENCE: CLOOLIBB
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SEG ID NO 3
SEQ ID NO 3
LENGTH: 28770
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                             TGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCAC
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IIILE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

IIILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28
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                                                            27962 GATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAATTG
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Pred. No. 1.1e-116;
1; Mismatches 1;
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ilarity 99.7%;
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Best Local Similarity
Matches 540; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: YE, Jame et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
CURRENT PELLING NUMBER: US/09/817, 198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SSCTWARE: FastsEQ for Windows Version 4.0
ELENGTH: 601
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Pred. No. 1.1e-116;
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Matches 599; Conservative
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ORGANISM: HOMO
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Patent No. US20020146758A1
GENERAL INFORMATION:
APPLICAMY: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.6e-104;
1; Mismatches 1;
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99.6%;
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241 AGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCCAGACTGTTAA
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OTHER INFORMATION: n = A,T,C
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Best Local Similarity 99.4%;
Matches 478; Conservative
                                                                                                                                                                                                                                      Sequence 303, Application Patent No. US20020136728A1
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Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLECLES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUCLES THEREOF
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001189
CURRENT PAPLICATION NUMBER: US/09/817,198A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 601
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                                                                                 CATGICITGAGGCCCAGACIGITAAGCAGGCICIGCIGGCCIGIITACICGICACCACCI
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Pred, No. 2.1e-99;
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99.8%;
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516; Conserv
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ORGANISM: HOMO
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                                                                                                         TTCGTGTACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAAC
GCAGGCTCTGCTGGTCTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACTCCA
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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Muscapher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IT
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IT
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SEQ ID NOS: 1789
SEQ ID NOS: 1789
SEQ ID NO 303
SEQ ID NO 303
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GENERAL INFORMATION:
APPLICANT: King Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: W. Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT APPLICATION NUMBER: US/10/033,528
SOFTWARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 303
LENGTH: 481
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NAME/KEY: misc_feature
LOCATION: 417, 461

OTHER INFORMATION: n = A,T,C or G
US-10-033-528-303
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Best Local Similarity 99.4<sup>†</sup>
Matches 478; Conservative
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ORGANISM: Homo sapiens
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Pred. No. 3.9e-83;
); Mismatches 2;
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APPLICANT: Horrigan, Stephen;
TITLE OF INVENTION: Cancer Gene Determination and;
TITLE OF INVENTION: Cancer Gene Determination and;
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEO ID NOS: 583
SOFTWARE: PATENTIN VETSION 3.0
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                                                                                                                                                  Sequence 26, Application US/09964824A Patent No. US20020102531A1
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Best Local Similarity 99.3%;
Matches 451; Conservative
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45 ATGGCGAAGCAGTACGATGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGC
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APPLICANT: MAYERS, Rachel
TITLE OF INVENTION: 42705, 23224, 27423, 32700, 32712, No. US20020009804Alel
TITLE OF INVENTION: Human G-Proteins
FILE REFERENCE: 35800/209285
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
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                    APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Bacriocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Stolk, John A.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS NO COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT FAPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                       Length 310;
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                                                                                                                                                                                                                                                                                                                                   Query Match 9.4%; Score 306.8; DB 9; Best Local Similarity 99.4%; Pred. No. 1.6e-55; Matches 308; Conservative 0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 624
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Matches 318; Conservative
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CORGANISM: homo sapiens
US-09-794-257-9
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CORGANISM: Homo sapiens
US-10-046-935-1930
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US-09-794-257-9
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Gaps

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APPLICATE: Meyers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1
TITLE OF INVENTION: Human G-Proteins
TITLE OF INVENTION: Human G-Proteins
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT APPLICATION NUMBER: 60/185,606
PRIOR APPLICATION NUMBER: 60/185,606
PRIOR FILING DATE: 2000-02-29
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1 ATGGCGAAGACGTACGATTATCTCTTCAAGCTCCTGCTGATCGGCGACTCGGGGGTAGGC
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llarity 65.6%; Pred. No. 1.1e-36;
Conservative 0; Mismatches 167;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09794257; Patent No. US20020009804A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (18)...(641)
US-09-794-257-7
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Matches 318; Conserv
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Sequence 885, Application US/09834975

Sequence 885, Application US/09834975

Patent No. US20020110815A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Brown, Jeffrey

APPLICANT: Bolt, Andrew

APPLICANT: Pandrew

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS

TITLE OF INVENTION: OF HUMAN CANCERS

TITLE REPERENCE: MRI-016B

CURRENT APPLICATION NUMBER: US/09/834,975

CURRENT APPLICATION NUMBER: 60/197,538

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 1046

SOFTWARE: FEALSEED FOR Windows Version 4.0
                                                                                                                                                                                                                            ATCTGGGACACTGCAGGCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG 284
                                    GCCCAGGGGATATTTTGGTCTATGACATTAGCAGCGGGGCGCTCTTACCAGCACATCATG 344
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; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-885
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ORGANISM: Homo sapiens
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Sequence 879, Application US/09834975

Patent No. US20020110815A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Boit, Andrew
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION: OF HUMAN CANCERS
TITLE REFERENCE: MRI-016B
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 879
LENGER: 2497
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ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGCCATCAAAGTGCGGATACAG
                  ATCTGGGACACTGCAGGGCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGG
                                                                                                                                                                                      AAGTGGGTCAGTGACGTGGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGG
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llarity 65.6%; Pred. No. 1.5e-36;
Conservative 0; Mismatches 167;
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; LCCATION: (1)...(2497)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-879
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 318; Conserv
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US-09-834-975-879
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Search completed: November 17, 2002, 20:38:39 Job time : 194 secs
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APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: With Harden, Christophe
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GRRES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SSECTIORS: FastsEQ for Windows Version 4.0
SSEQ ID NO 894
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Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
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; OTHER INFORMATION: n = A,T,C or
US-09-834-975-894
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Matches 318; Conservative
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ORGANISM: Homo sapiens
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Run on:

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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04-FEB-2000;
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20000US-0241809. 2000US-0244617. 2000US-0246477. 2000US-0246475. 2000US-0246477. 2000US-0246477. 2000US-0246477. 2000US-0246523. 2000US-0246525. 2000US-0246525. 2000US-0246528. 2000US-0246532. 2000US-0246609. 2000US-0246610. 2000US-0246611. 2000US-0246613. 2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0249212. 2000US-0249213. 2000US-0249216. 2000US-0249217. 2000US-0249218. 2000US-0251988. 2000US-0256719. 2000US-0251479. 2000US-0251856. 2000US-0251869. 2000US-0251869. 2000US-0249299 2000US-0249300 2000US-0249215 2000US-0251030 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 7-NOV-2000; 7-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-DEC-2000; 05-DEC-2000; 17-NOV-2000; 7-NOV-2000; 05-DEC-2000;

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, WPI; 2001-483426/52 human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and Nucleic acids encoding useful for preventing, metastasis metastasis

Disclosure; SEQ ID NO 37097; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to

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supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially aconcers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54921 to AAK54950 and AAW82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                        3100 TGCCAGGGGAGAGGAGGACACTGGACTAACCTGTGCCTTTGGTTTCCAGTCATTCAC 3041
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                                                                                                                                                                                                                                             2740 GAGGGGTCTGTCTGTCATCTCAAGCACCCCTGTCCCCAGCCCGTCCAGCCGTGGAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGTCTCACCATCCCGCACCCACCAGACAACAGGCCTGGGGGTCCAGGCCACTTTC
                                                                                                                Score 2696.6; DB 22; Length 3240;
Pred. No. 0;
0; Mismatches 34; Indels 0;
                                                                                               Sequence 3240 BP; 713 A; 882 C; 887 G; 758 T; 0 other;
                                                                                                                 82.8%;
98.8%;
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Matches 2717; Conservative
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| QQ | 2260 | |
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| QY | 1373 | CGGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGAC |
| Dβ | 2200 | GCAACCAGGAATCCTCGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCGA |
| Qy | 1433 | GCCCTTGCTTGGCTGCCCGCCTCTTTGGGGAACTGAGCTCAGAGGCAGG 149 |
| gg | 2140 | ltgcccttgcttggctgcccgcctgccttttggggaactgagctcagaggcag |
| ۷ <u>٥</u> ۲ | 1493 | TGCTTCAGAGAAGGAAACAAAATGAGGGTGGCAGGATAAAAAGTCACCTCCATTCTCT 1552 |
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| S 2 | ו מ | ACCICCCATGCAGCATGAACACAATTTCTCTCCACCACGCTCCCAAATTTAAAGATGTGG 1961 ACCICCCATGCAGCACGAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGG 1961 |
| Qy | 1613 | CCAAGGCCTGTGGGTACTCCAGGGGCAAGGAAGGACCCTGGGGGTCAGTGACACTGTCAG |
| qq | 1960 | ACCAAGGCCTGTGGGTACTCCAGGGGCAAGGAGAGCCCTGGGGGTCAGTGACACTGTCAGG 1901 |
| Qy | 1673 | CCAACCATGCACTCCACAAAGGGGAGCATTTGGAAATGAAGGACTAGCTCCTATGTATCA 1732 |
| ΩĐ | 1900 | CAACCATGCACTCCACAAAGGGAAGCATTTGGAAATGAAGGGACTAGCTCCTATGTAT CAACCATGCACTCCACAAGGGAAGCATTTGGAAATGAAGGACTAGCTCCTATGTAT |
| Qy | 1733 | GGTTAAGAGCAAGGGAGAGCTGGCCAGGGACAGCAGTTTGCACAGCAGAGGGGAATGTAG 1792 |
| qq | 1840 | CAGGGACAGCATTTGCACAGCAGAGGGGAATGT |
| QY | 1793 | CAACAGCAGGCCTCCTAGGCCCCCATCTTCTTAGGTAAGAAGAGCATTTCCTCA 1852 |
| QQ | 1780 | CCCATCTTCCATTTCTTAGGTAAGAAGAGCATTTCCT |
| QY | 1853 | GACTCCCAGGCGGAGGACTGAGCCTAGCCTTCAGCAAGGTTCTCCTGGGACCCAAA 1912 |
| QQ | 1720 | CCAGGCGAGGACTGACCTACACCAACCAAGGTTCTCTGGGAC |
| QY | 1913 | GTTTATGGGAGAGAGGCAAAGACTTCATGGGAAGAGAGAG |
| QQ | 1660 | AGAAGGGCAAAGACTTCAT |
| Qy | 1973 | GCTTGGTGCTGTTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGCCCTCTACCTCTG 2032 |
| QQ | 1600 | CTTGGTGCTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGCCCTCTACCTCCT |
| QY | 2033 | TAGGCTTGAGGGTTTGCCAACCACACTGTGGCTACAGGTGGA |
| QQ | 1540 | GAGGGTTTGCCAACCACACTGTGGGCTACAGGTGGAGG |
| QY | 2093 | CICCAGAGIGCTAIGITCAGGAAGTITCTTTAACCCCATAIGGCCCAAGAGTAGCTCGTA 2152 |
| QQ | 1480 | CAGAGTGCTATGTTCAGGAAGTTTCTTTAACCCCATATGGCCCAAGAGTAGCTCGT |
| QY | 2153 | GAGGCCCTTTAAAGACGGAACAAGTAATTTACCAGTTCTACTGGGGTTCCTGC |
| QΩ | 1420 | AGGCCCTTTAAAGACGGAACAAGTAATTTACCAGTTCTACTGGGGTTCCTGCC |
| Qy | 2213 | AGGAAGAGGGTCATTCTTAAGCCACACATT |
| QQ | 1360 | CCAAGGTGGGCGAGGCCTAGGAAGAGGTCATTCTTAAGCCACACATTAGCTGCACT |
| QY | 2273 | GTGGCTGCAGCCAAAACAAAGAACTGGGTGTTGAGTATT |
| qq | 1300 | GGCTGCAGCCAAAACAAAGAACTGGGTGTTGAGTATTCATCAACTAAGAACCAAAA |
| ΟŸ | 2333 | CCAGGGCACTCATATGTGAAGGATAAGAACCTCACTTACTCCTTACTCCTCAAAAAGAAGTG 2392 |
| QQ | 1240 | GGGCACTCATATGTGAAGGATAAGAACCTCACTTCCTTACTCCTCCAAAAAGAAGT |
| ΟŸ | 2393 | GGGAAAGAACCATCAAACCTTTCCTCGCTTACCAAACCAGGAAAACAGCAGGAGAGG 2452 |

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vulnerary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonisant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antivati antibacterial; antidactial; antidagal; antithemmatic; antithyroid; antithacamemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        open reading frame; ORFX; detection; cytostatic; hepatotropic; ary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
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1180 GGGAAAGAACCATCAAACCTTTCCTCCTGACTTACCAAACCAGGAAAACAGGAGGGGG 1121
                                                                                                                     1060 AGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGGAC 1001
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                                                                                                 2513 AGTTGTAAATCACTGGCTAATGAGAAAAGGAGACAGCTAACTCTAGGATGAAGCTGTGAC
                                                                                                                                                                     2573 TAGGCTGGAGTTGCTTCCTTGAAGATGGGACTCCTTGGGTATCAAGACCTATGCCACATC
                                                                                                                                                                                                                                                                                                                                            880 GAGAAGTTATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTCAGCTTTCCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                 Human ORFX ORF1368 polynucleotide sequence SEQ ID NO:2735.
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepstotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining pathological conditions associated with an OREX-associated disorder. The nucleic acids and nucleic acids may be used to treat cancers, propliferative disorders, neuroders and nucleic acids may be used to treat cancers, propliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferative disorders, neurodegenerative disorders, osteoarthrits, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTTGAACTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coaqulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders'and cardiovascular disease -
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Pred. No. 0:
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B (NM_000497), CXP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_000497), OCLN (NM_000538), TANRRI (NM_000378), ONE (NM_003380), NM_01990, NM_019902, NM_019902, NM_019903, NM_019903
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1364 TAGGAGGGAAACAGCAACCGGGGAGTCCTCGAGCCTGGGGGCTGCCCTACCTCTACCCATT 1423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1428 TAGGAGGAAACGGCAACCAGGGAGTCCTCGAGGCCTGGGGCTGCCCTACCTCTACCCATT
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which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPS (single nucleotide polymorphisms) of the 87 sequences. The oligomers may also be used as PCR primers on the set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement.
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                                                                                                                                of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                         Score 1192.8; DB 24; Length
Pred. No. 5e-279;
0; Mismatches 472; Indels
                                                                                                                                                                                  Sequence 7924 BP; 2087 A; 83 C; 2037 G; 3717 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxeemia, Alzheimer's disease, Alzh. epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
1861 TGTGTTTCGGGTTTATATATGAATTGTGAGTAGGGTTTATTTTATTTTAAATATAGATGTT 1920
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                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiliflammatory; cancer; antidiabetic; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilopsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                                                          Human immune system associated gene SEQ ID NO:
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01-SEP-2000; 2000DE-1043826
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            GATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGC
                                    GATGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGT
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDHG (NM_000693), CYP11A (NM_000781), CYP11B1 (NM_000497), CYP333 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_0004996, NM_019900, NM_019901, NM_019902, NM_019808, NM_019809) and their complementary sequences, or a sequence (S1) chosen from 87 sequences and their complements. The chemical pretreatment to convert cytosines (but not methyl-cytosines) into uracilis. Also included are an oligomer (II) in particular an oligomer capture of a beptide nucleic acid (PNA)-oligomer, comprising in cach case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in a rary for analysing diseases associated with the methylation state (CG) and/or detecting SNPS (single nucleotide polymorphisms) cof the 87 sequences. The oligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence capta for this patent directly from MIPO at the complement of the printed specification, but was obtained in electronic of the printed specification, but was obtained in electronic for the printed specification, but associated for an electronic of the printed specification, but associated for an electronic of contine directly from MIPO at the complement of the printed specification, but associated for an electronic of the printed specification, but associated for an electronic of the printed specification, but associated for an electronic form part for the printed are an electronic form part for the printed are an electronic form part for the printed and the electronic form part for the printed and the electronic form part for the electronic form part for the e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 152; 24pp; English.
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30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                     Piepenbrock C,
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| QY 2778 TTTCTCTCCTAGCCCCTCAGGAAGAGGACTATTTGTACTGTACCCTAGGGGTTCT 2837 b 6422 TTTCTCTCCTAACCCCTCAAAAAAAAAAAAAAAAAATTATT | 3018 TGGCCTGTTACTCGTCACCACCTCTGCACCTGCTGTGTGTG | ABL34139 standard; DNA; 7924 BP. ABL34139; 26-MAR-2002 (first entry) Human immune system associated gene SEQ ID NO: 2112. Human; immune system disease; cytosine methylation; antias antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologica antinheumatic; antiathrill; antidiabetic; antisporiatic; antihlammatic; antiathrill; antidiabetic; antisporiatic; antinheumatic; antiathrill; antidiabetic; antisporiatic; anticheumatic; antidiabetic; anti | KW gene; ds. XX Signes; ds. XX Homo sapiens. XX My200200928-A2. XX WX WC200200928-A2. XX WX WC200200928-A2. XX WX WX WC20000528-A2. XX MY2002 Signes; discrete |
|---|--|--|--|
| 162 ACAAAAAAACCCTAAAAATCAATAACACTATCAAACCATACCATACCACC | | 111 | OY 2418 CLIANTIACLARALACARCARARARATARCTCARARATTARCARACACTOR 2477 Db 6782 CCTAACTTACCAAACAAAAAACACAAAAAAAAAAAATACTCAAAACTTAAAAAA |

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                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxeamia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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ss 512; Indels
           NO 2112; 32pp + Sequence Listing; German
                                                                                                                                              Sequence 7924 BP; 1973 A; 83 C; 1827 G; 4041 T; 0 other;
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0; Mismatches
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Best Local Similarity 74.1%;
Matches 1468; Conservative
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            Claim 1; SEQ
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2837 6363 6123 2477 2657 2777 6423 2177 ACACGCCCACTACTCCTAAAACCTCCCTATTAAACGAAAAACTTCGTATAACTA TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTTTA CCCTAAAACTTTTAATAACCTAAAACATATCTTAAAACCCAAACTATTAACCAAACTAC GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTG TITCTCTCCTAGCCCCCTCAGGAAGAAGACTATATTTGTACTGTACCCTAGGGGTTCT GGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCCAT AAAAAAAAAACATAAAATCAAAATTCTATAAACTAATAAACCCTATCCACAAAAACCAT GACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCA CCCTAAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCCAGACTGTTAAGCAGGCTCTGC TTCTTTAACCCCATATGGCCCAAGAGTAGCTCGTAGGAGGCCCTTTAAAGACGGAACAAG GAGGGTCATTCTTAAGCCACACATTAGCTGCACTGCGTGGCTGCAGCCAAAACAAAGAAC AAAAATCATTCTTAAACCACACATTAACTACACTACGTAACTACAAAAAAC AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAAACCTTTCCT CCTGACTTACCAAACCAGGAAAACAGCAGGAGAGGGTGGCTCAGGACTTAGGGACAGGGT 6782 CCTAACTTACCAAACCAAAAAAACAACAAAAAAAATAACTCAAAACTTAAAAACAAAAT ATAGCTTAGATGGTGGAAAGCAAAGGAGAGCAGGAAGTTGTAAATCACTGGCTAATGAGA AAAGGAGACAGCTAACTCTAGGATGAAGCTGTGACTAGGCTGGAGTTGCTTCCTTGAAGA TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGGCTAGGGAAGTAGGTGA TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTC TAATTTACCAGTTCTACTGGGGTTCCTGCCCACCGTCCCAAGGTGGGCGAGGCCTAGGAA 2658 2838 6362 2898 6302 6242 6182 3078 6122 6062 6602 2718 2778 2958 3018 3138 2478 6722 2538 6662 2118 7082 2178 7022 2238 6962 2358 2418 2598 QQ g ΟŊ g ōλ g ŏ a οy Db δy g á g δy qq ŏ q δ g δ g δ qq ò g g g g g Qγ QΥ Qγ 9 δý

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   Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antinfilammatory; anti-HIV; antibacterial; antinfilammatory; cancer; immune system disorder; rheumatoid arthritis; infilammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; chromosomal abnormality; Dwn syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                cDNA encoding novel signal transduction pathway protein, Seq ID 88
                                                                                                       AAS27053 standard; cDNA; 2021 BP
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2000US-0198123.
2000US-0205515.
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2000US-0214886.
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The invention relates to novel isolated polypeptides (I), and displaced diagnosing, preventing and treating diseases including immune system disponders (e.g. congenital and acquired immunodeficiencies, autoimmune classorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. theumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, infectious diseases classorders, primary haematopolotic disorders, myeloproliferative disorders (e.g. dasorders (sickle cell anaemia), myeloproliferative disorders (e.g. Alzhelmer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. strongers), renal abnormalities (e.g. alzhelmer's disease, Parkinson's disease), chromosomal abnormalities (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders; (e.g. arrhythmia) epithelial cell proliferation, endocrine disorders, in wound healing, epithelial cell proliferation, endocrine disorders; (as stimulators of B-cell responsiveness to pathogens, activators of as stimulators of B-cell responsiveness to pathogens, activators of tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (ADDS). AAS2096-AAS2080 represent novel signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
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2000US-0250391.
2000US-0251030.
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2000US-0249245.
2000US-0249264.
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pathway protein coding sequences and PCR primers of the invention

ö Gaps 97 GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA ö 9; Indels Pred. No. 1.8e-271; 0; Mismatches 9; 35.6%; Score 1160.6; 99.2%; Pred. No. 1.8e Conservative Similarity Best Local Simi Matches 1166; 38 62 86 셤 δý g ò

DB 22; Length 2021;

Query Match

937 997 781 841 877 901 961 421 457 541 577 601 637 697 721 757 817 241 277 301 337 361 397 481 517 661 998 CCATCCCGCACCCACCAGACAACAGCCAGGGCTGGAGTCCAGGCCACTTTCAGCTGCTCC 842 IGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGTCTTTTCAG 878 TGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGGCTTCTTCAG CCATCCCGCACCCACCAGAACAACAGCCAGGGCTGGAGTCCAGGCCACTTTCAGCTGCTCC TTTCTCCGTGCATCGTGTCTTCTCTGCTTTTTTCTCTCTTTCCCCCACTTCTCTTTCTCT GACCCCTCCCCTCCGGTGCGTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCGTGTGTC 422 GCAGAAACGGCAGGTGGGAAGAGAGAGAGGGCCAGCAGCTGGCGAAGGAGTATGGCATGGA 638 TGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGCCAAACCCGAGGGCCCAGCGAACTC TCAGGAGGCCCGTGGGCAGACAGGGGAGCCGGGGGCTTTGCCCTGCTGCTGTCCTCTCGTG CCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCACGATGTGCCGCAAGCACTGTCTCA 482 CTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGAC 602 TGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGGCAAACCCGAGGGCCCAGCGAATTC CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG GCAGGAGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGCCCAGGGGATATTTTT GGTCTATGACATTAGCAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGT GGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGA 662 TICGAAAACCIGCIGGIGCIGAGICCIGIGIGGGGCACCCCACACGACACCCCICITCCC GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG CTGCTGTGTGCAGCTCGCTCTTTCCTCCTCGTA 1212 CTGCTGTGTGCAGCTCGCTCTTTCCTTCCTA 1176 1082 1142 1178 782 902 962 1118 722 158 182 218 242 278 302 362 122 g g a δy g δy g ò g δy g δ g δ g οy g δ g οy 셤 ð g ò g ŏ g g q ŏ g δ ò Q

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3017

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612

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chromosomal abnormality; Down syndrome; ischaemia; renal disorder; carditovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                            2658 TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTC 2717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3078 GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACTTCGTGTACTG 3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3138 TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTAAACACAGATGTTTA 3197
                                                                                                                                                                             cDNA encoding novel signal transduction pathway protein, Seg ID 507.
                                                                TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGA
                                                                                                                                314 TGCCAGCCTCAAGTCTGTCTTCAGCCAGGACTTGAGAAGTTATATTGGGCAGTGGCTC
                                                                                                                                                                                              2778 ITTCTCTCCTAGCCCCCCCAGGAAGGACTATATTTGTACTGTACCCTAGGGGTTCT
                                                                                                                                                                                                                                                                                                          2838 GGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCCACAAGGGCCAT
                                                                                                                                                                                                                                                                                                                             GACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAAGCAGGCTCTGC
                                                                                                                                                                                                                                                                          AAS27472 standard; cDNA; 566 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel polypeptide fragments (I) and the polynucleotides (II) that encode them that are highly expressed in a human bladder tumour and which have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for treatment of bladder cancer, to directly treat this form of cancer (including expression from gene therapy vectors) or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a capture isolated from a human bladder tumour cDNA library which encode the proteins represented in AAY66143·Y66198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences expressed in bladder tumor tissue, and derived polypeptides, for treatment of bladder tumor and identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2358 AGAACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAAACCTTTCCT 2417
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                                                                                                                                                                           tag; human; bladder; tumour; cancer; cytostatic;
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                                                                                                                                           Human bladder tumour cDNA library derived EST 12
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                                                                                                                                                                                            treatment; gene therapy; EST; ss.
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                                          AAZ24400 standard; cDNA; 895 BP
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                                                                                                          (first entry)
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                                                                                                                                                                           Expressed sequence
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es 879; Conserv
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| PR 29-SEP-2000; 2000US-0236369. PR 29-SEP-2000; 2000US-02363309. PR 29-SEP-2000; 2000US-02363370. PR 02-OCT-2000; 2000US-0237031. PR 02-OCT-2000; 2000US-0237031. PR 02-OCT-2000; 2000US-0237031. PR 13-OCT-2000; 2000US-023937. PR 13-OCT-2000; 2000US-023935. PR 13-OCT-2000; 2000US-024985. PR 20-OCT-2000; 2000US-0241826. PR 20-OCT-2000; 2000US-0241821. |
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| 2000US-01312. 2000US-0179065. 2000US-0186528. 2000US-0186528. 2000US-018654. 2000US-018874. 2000US-0198123. 2000US-019818. |
| 17 - JAN - 2001. 17 - JAN - 2001. 24 - FEB - 2000. 24 - FEB - 2000. 24 - FEB - 2000. 25 - MAR - 2000. 26 - MAR - 2000. 27 - MAR - 2000. 28 - JUN - 2000. 29 - JUN - 2000. 20 - JUN - 2000. 20 - JUN - 2000. 20 - JUN - 2000. 21 - JUN - 2000. 22 - JUN - 2000. 24 - JUN - 2000. 25 - JUN - 2000. 26 - JUL - 2000. 26 - JUL - 2000. 27 - JUN - 2000. 28 - JUN - 2000. 28 - JUN - 2000. 29 - JUN - 2000. 20 - JUN - 2000. 20 - JUN - 2000. 20 - JUN - 2000. 21 - JUN - 2000. 22 - JUN - 2000. 23 - JUN - 2000. 24 - JUN - 2000. 25 - JUN - 2000. 26 - JUN - 2000. 27 - JUN - 2000. 28 - JUN - 2000. 28 - JUN - 2000. 29 - JUN - 2000. 20 - J |
| 0 × 7 × 7 × 7 × 7 × 7 × 7 × 7 × 7 × 7 × |

Ruben SM; SENOME SCI INC. sh SC, 60/50. ABK44752 standard; cDNA; 481

RESULT 10

ABK44752

ABK44752;

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disorders (e.g. congenital and aquired immunodeficiencies, autoimmuno disorders (e.g. congenital and aquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant respections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, in memorphic and concernities and cherry blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal aborders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal aborders (e.g. alzheimer's disease, Parkinson's disease), chromosomal aborders (e.g. alzheimer's disease, parkinson's disease), chromosomal aborders (e.g. alzhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. addisorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. e.g. ecquired immune deficiency syndrome (Ands) AAS26976-AAS27800 represent novel signal transduction cpathway protein coding sequences and PCR primers of the invention.
                                                                                                         Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated polypeptides (I), and polynucleotides (II). (I), (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system
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                                                                                                                                                                                                                                                   disorders and neuronal disorders
P-PSDB; AAU17555
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                                                                                                                                                           148 CCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAA 207
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                       Gaps
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                                             GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTACGA 61
                                                                                        TGTGCTGTTCCGGCTGCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGTGTG
                                                                                                                                                                                              28 GCCCGCTGCCCGCCCGCAGTTCCCGGCCCCGCTGGCCCAGTCATGGCGAAGCAGTACGA
                                                                                                                                                                                  GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGG
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                                                                                                                                                                                                                               GCAGGAGATACCAGACCATCACAAAGCAGTACTATCGGCGGCCCAGGGGATATTTTT
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Length 566;
                      Indels
 DB 22;
16.4%; Score 534.2; DB 22 98.9%; Pred. No. 1.3e-119;
                     2; Mismatches
                      533; Conservative
             Similarity
 Query Match
           Best Local
Matches 53
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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynuclectide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK4450-ABK46237 represent coding sequences of human colon tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer -
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                                                                                                                                                                                   vaccine; colon cancer; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 481 BP; 111 A; 113 C; 130 G; 125 T; 2 other;
                                                                                                                         SEQ ID No 303.
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                                                                                                                         cDNA encoding colon tumour protein,
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28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
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                                                          (first entry)
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                                                                                                                                                                                       colon tumour;
                                                                                                                                                                                                                    immunotherapy; gene;
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                                                                                                                                                                                                                                                                                                                                             WO200212328-A2.
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                                                          05-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                        2941
                                                                                                                                 3001
                                                                                                                                                                                          GTTAAGCAGGCTCTGCTGCTGTTTACTCGTCACCACCTCTGCACCTGCTGCTGTTCTTGAGA 3061
                                          300
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                          GTACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATAGGCCC
                                                                     2882 TATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAAATTGGGATTTTAG
                                                                                     GGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACT
                                                                                                                                                 Thyroid cancer related gene sequence SEQ ID NO:5329.
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ABL66992 standard; DNA; 463 BP.
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2000US-235711P.
2000US-235720P.
2000US-235840P.
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2000US-234052P.
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2000US-234567P.
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2000US-234924P.
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25-SEP-2000

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28-SEP-200
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the structure and/or actiona, clear collected actionactic cancer, infilitating ductal cancer, infilitating lobular cancer, squamous cell carcinoma, neuroendocrine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 463 BP; 116 A; 108 C; 110 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carcinoma, papillary carcinoma and Wilm's tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebner R,
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                                                         20000S-237173P.
20000S-23728PP.
20000S-23729PP.
20000S-237295P.
20000S-237316P.
20000S-237425P.
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2000US-237606P.
2000US-237608P.
2000US-244867P.
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Matches 451; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVAL-) AVALON PHARM.
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29-SEP-2000,
02-OCT-2000,
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Soppet DR,
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                                                                           3209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
ATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTTTACAAAATAAAGAT
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Pred. No. 4.1e-66;
                                                                                                                                                                               3210 TATTTCAAACCACCAAAAAAAAAAAAAAAAA 3243
                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                               AAT25457 standard; cDNA to mRNA; 320
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ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I)
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                                                                                                                           2991
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                                                  2872 TGATAGGCCCTATCCACAAGGGCCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAATT 2931
                                                                                                                                                                                              2992 GGCCCAGACTGTTAAGCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGC 3051
180
                                                                                                                                                            240
                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                241 GGCCCAGACTGITAAACAGGCTCTGCTGCTGTTTACTCGTCACCTCTGCACCTGC
                                                                      2932 GGGATTTTAGGGTGCAGCTACGCTCACCCTAAACTTTTGGTGGCCTGGGGGCATGTCTTGA
                                                                                                                                           Human; colon cancer; colon tumour antigen; cytostatic; vaccine; colon tumour metastatic antigen; diagnosis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon tumour antigen polynucleotide SEQ ID NO:1930
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                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                              ABL38341 standard; cDNA; 313
                                                                                                                                                                                                                                                                     TGTCTTGAGACTCCATCC 3069
                                                                                                                                                                                                                                                                                       301 TGTCTTGAGACTCCATCC 318
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20-FEB-2001; 2001US-270216P
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9.4%; Score 307; DB 24; Length 313;

Query Match

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Gaps

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Indels

2752 GATCAGGCAGGGTGCCATTCATTGTCTTTCTCTCCTAGCCCCCTCAGGAAAGAAGACTA 2811

0; Mismatches

Matches 314; Conservative

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Local Similarity

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Claim 1; Page 805; 1963pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; growth factor; hemactopolasis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; metolide cell disorder; lymphold cell disorder; asthma; atthritis; chronic inflammatory condition; proliferative retinopathy; atthrosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                  3063
                                                                                                                                                                                                                                                                                                                                                                                                                                             3123
                                                                                                                                                             2884 TCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGG 2943
                                                                                                                                                                                                                                                          3003
                                                                  2824 ACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTA 2883
                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CCATCCAGCCCCAGGCACCCCCCTGAGCCTCCACTATCTCCCTGTGAGCGTG 300
                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                            1 ACCCTAGGGGTTCTGGAAGGGAAACATGGAATCAGGATTCTATAGACTGATGGGCCCTA
                                                                                                                                                                                       3004 TAAGCAGGCTCTGCTGGCCGCTGTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTG
                                                                                                                                                                                                                                                          2944 TGCAGCTACGCTCACCCTAAACTTTTGGTGGCCCTGGGGCATGTCTTGAGGCCCAGACTGT
                                                                                                                                                                                                                                                                                                                                                                                               181 TAACCAGGCTCTGCTGGCCTGTTTACTCGTCACCTCTGCACCTGCTGCTGTCTTGAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:936.
ed. No. 1.4e-64;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human rab8 homologue-encoding cDNA,
  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA09160 standard; cDNA; 1986 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0496914.
  99.08;
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                          308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3124 AACTTCGTGTA 3134
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; ABB11916.
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  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                          Matches
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ABA09160
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Sequences ABAB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

CC uncleotide of the invention, methods of identifying compounds which control to polypeptides of the invention. Although novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; immunomodulatory activity; tissue growth activity; concentrated activities; or may be encounted and activities; or may activity; involved in oncogenesis, cancer cell proliferation or metastasis.

CC chemotactic or chemokinetic activities, hadmostatic, thrombotic or thrombolytic activities, receptor or ligand activities; or may be conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include careers, hematoposited disorders (e.g., metalions or ameliorating medical carefrail is schemial, bound disorders (e.g., osteoporosis), and abnormal activities may be used to promote wound repair (or nucleic acids encoding them) may be used to promote wound repair indications incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, and becent and fungal infections in addition to immune disorders to promote call growth. Polypeptides with prowth factor activity may be used in cell culture to give rise to neuropeptides with growth factor activity may be used in cell conditions and cells in culture to give propage to element of the promote cell growth factor activity may be us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening techniques. The present sequence represents a CDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 ATGGCGAAGACCTACGATTACCTGTTCAAGCTGCTGATCGGGGACTCGGGGGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 AAGACCTGCCTGCTGCCGCTTCACCGACAACGAGTTCCACTCCTCGCACATCTCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGGTGTTGACTTTAAGATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 160;
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67.0%; Pred. No. 2.8e-45;
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Best Local Similarity
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Search completed: November 17, 2002, 18:15:04
Job time : 471 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea: endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; restinancy cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
379 AACAAGTGTGATGTGAATGACAAGAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCC 438
                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                           AAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HCGMA67 cDNA, SEQ ID NO:290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 290; 2922pp; English.
                                                                                                                                                                                                                                                                                  ABQ54410 standard; cDNA; 2411 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                       499 GCATT 503
                                                                                                                            525 TCATT 529
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                                                                                                                                                                                                                                                                                                                             ABQ54410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                       RESULT 15
ABQ54410
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respiratory disorders, neurological disorders, gastrointestinal disorders
             and urinary system disorders. Ovarian antigen polypeptides and polypucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polypucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 GGGACTCGGGGGTGGGGAAGACCTGTGTCCTGTTCCGCTTCTCCGAGGACGCCTTCAACT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGGCAGCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAAACAAGTGCCTGCACCA 507
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACTCCGGGGTGGGCAAGACCTGCCTGCTGTGCCGCTTCACCGACAACGAGTTCCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 228.4; DB 24; Length 2411; Pred. No. 4.3e-45; 0; Mismatches 171; Indels 0;
                                                                                                                                                                                                                                                        Sequence 2411 BP; 600 A; 671 C; 583 G; 547 T; 10 other;
                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            Query Match 7.0%;
Best Local Similarity 65.9%;
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November 17, 2002, 16:48:24 ; Search time 5516 Seconds (without alignments) 17184.162 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                               2054640 segs, 14551402878 residues
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19051)
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Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,

AL139022 AL139022.4 GI:14148954

human.

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | AL139022 | AX347040 | AX348436 | 14014CAA | | AX014147 | BC027769 Mus m | M83679 S | | AX334820 AC096084 | BC013790 | AC124556 | AX341683 Seque | | S53268 HOMO Sa | AF49894 | X56741 H.sapien | S53270 MEL=R | | M38391 Discop | AX23607 | BC020654 | AX236U/6 | AX285074 | AX285080 | AX285089 | AXZBOUST SEQUE | AL833365 | U53475 Rattus | MB3677 Spragu | 244 O AFUSJO40 MUS | 347 1 Continuation | 292 AC027292 Homo | 396 BC000896 | 223 AK023223 Homo | 1620 AL136650 Homo | AIU696/1 DIOSC 7 D84347 Drosoph | ALIGNMENTS | |
|------------|-------------|----------|----------|----------|-----------|---------|----------|----------------|----------|-----|----------------------|-------------|----------|----------------|------|----------------|---------|-----------------|--------------|-------|---------------|------------|----------|----------|----------|----------|----------|----------------|----------|---------------|---------------|--------------------|--------------------|-------------------|--------------|-------------------|--------------------|------------------------------------|------------|----------|
| | DB ID | NS0 | | AX340 | | 6 AX399 | | 0 | 0 | | | 10 BC013790 | | | | | | | 0 | > | | 6 AX236078 | | | | | | | | 0 | 0 | TO AFOS | | 2 AC027 | | AK02 | HSWB | 3 AYU69 3 D8434 | AI | |
| | Length | 190517 | 7924 | 1924 | 1007 | 1054 | 895 | 3139 | 945 | 481 | 403 | | 257226 | 313 | 2048 | 1980 | 624 | 099 | 638 | 760 | 765 | 624 | 1128 | 1265 | 2497 | 2497 | 2497 | 2027 | 3110 | 740 | 991 | | 110000 | | 1029 | 3533 | 3521 | 2210 | | |
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| | Score | 96 | 82 | 7 0 | 2 5 | 20 | 99 | 8 | 77 | 77 | א כ | 416.4 | 78 | ო : | 3.4 | 230.6 | 229 | 229 | 227.4 | 2.477 | 218.2 | 217.8 | 217.8 | 217.8 | 217.8 | 217.8 | 217.8 | 217.8 | 216.2 | 211.4 | 203.2 | 1001 | 198.6 | 198.6 | 198.4 | 198.4 | 196.8 | 196.6 | | |
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OY 833 GAGGGGTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCCGTCCACCCTGGAGTGGT 892
Db 157979 GAGCGGCTCTGCTGTCATCTCAAGCAGCCCCTGTCCCCAGCCGTCCACCCTGGAGTGGT 158038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 TGGCATGGACTTCTATGAAACAAGTGCCTGCACCAACCTCAACATTAAAGAGTCATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 TGCCAGCAATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGAGGCAAACCCGAGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGAACTCTTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGCACCCCACACGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 CCTCTTCCCTCAGGAGGCCCGTGGGCAGAGAGAGGGGGAGCCGGGGGCTTTGCCCTGCTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCCGGCCTGGCCCTGA
                                                   identified using the e-PCR software (G. Schuler)" 47222. .47411
                                                                                                                                                                                                                                                                                                                                                                                                             dbsrs:srs40906
Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dbSTS:STS22552
Identified using the e-PCR software (G. Schuler)"
173833. .174012
/note="matching EMBL:G27797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dbSTS:STS4675
Identified using the e-PCR software (G. Schuler)"
a 43175 c 42572 g 52023 t
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164135. .164257
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                                                                                             EMBL: AA165116
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/note="matching EMBL:R10900
/note="matching EMBL:L00635
RHdb:RH53755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.8%; Score 2696.6; Best Local Similarity 98.8%; Pred. No. 0; Matches 2717; Conservative 0; Mismatches
                                                                                                                                                                                          /note="matching EMBL:G07650
                                                                                                                                                                                                                                                                                                                                                                                     /note="matching EMBL:W56308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="matching EMBL: Z39818
                                                                                                                                                    Identified using the 128322. .128437
                                                                           47222. .47411
/note="matching
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                                                                                                                 RHdb:RH48540
dbSTS:STS41599
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                                       dbSTS:STS12411
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                                                                                                         Direct Submission
Submitted (17-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On May 18, 2001 this sequence version replaced g1:10798506.
                                                                                                                                                                                                                                                                                                                             Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dbsTs:sTs48849
Identified using the e-PCR software (G. Schuler)"
30401. 30624
Anote=matching EMBL:R42375
RHdb:RH69913
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//note="matching EMBL:AA053315
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Identified using the e-PCR software (G. Schuler)"
44712. .44832
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44712. .44852
/note="matching EMBL:L00635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percentage of bases with a quality value >= 40 : 99 %.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 2.0
Quality coverage: 7.14x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                Center: Genoscope / Centre National de Sequencage
Center code: GS
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Identified using the e-PCR software (G. 43552, 43739
/note="matching EMBL:239082
RHdb:RH25206
                                                                                                                                                                                                                                                                      Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22163. .22307
/note="matching EMBL:H99639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="R-840119"
/clone_lib="RPCI-11"
22163. .22307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overall quality chart:
Range: bases
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                                                                       2 (bases 1 to 190517)
Genoscope.
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| 952 158098 1012 158158 1072 1158218 1132 | 192 5833 252 - 252 - 312 312 5845: | 1372 158518 1432 158578 1492 158638 1552 | 612 5875(672 5881(732 | 1792 158938 1852 158998 1912 159058 1972 |
|---|--|--|---|--|
| CTTCTTCAGCCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCACGATGTGCCGCAAGC CTTCTTCAGCCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCCCACGATGTGCCGCAAGC CTTCTTCAGCCTGTTTCCCCACGCCACAGGCCTGCTACGACCCCCCACGATGTGCCGCAAGC ACTGTCTCACCATCCCGCACCCACCAGCAAACAGCCAGGGCTGGAGTCCAGGCCACTTC ACTGTCTCACCATCCCGCACCCACCAAACAGCCAGGGCTGGAGTCCAGGCCACTTC ACTGTCTCTCACCATCCCGTGCATCGTGTCTTCTCTCTTTTCTCTCTTCCCCCCACTTC AGCTGCTCTTTCTCGGTGCATCGTGTTCTTTTTTTTTT | | ### ### ############################## | COTGCAGCATGAACACTTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTG | GGTTAAGAGCAAGGGAAGCTGGCCAAGGACAGCAGACACAGCAGGGGAATGTAG [|
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Diagnosis of diseases associated with the immu Patent: WO 0200928-A 2112 03-JAN-2002;
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Location/Qualifiers
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Best Local Similarity 74.1%; Pred. No. 4.1e-288;
Matches 1468; Conservative 0; Mismatches 512;
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(Homo sapiens)"
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83 c 1827 g 4041
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Best Local Similarity 74.1%;
Matches 1468; Conservative
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AX399903 1054 bp Sequence 74 from Patent WO0218424 AX399903

LOCUS DEFINITION ACCESSION

RESULT 6 AX399903

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                                                                                                                      Tang, Y.T., Asundi, V., Zhou, P., Xue, A.J., Ren, F., Zhang, J.,
Wang, J.R., Zhao, Q.A., Wang, D., Liu, C., Drmanac, R.T. and Wehrman, T.
Nucleic acids and polypeptides
Patent: WO 0218424-A 74 07-MAR-2002;
HYSEQ, INC. (US)
Location/Qualifiers
                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 8.2e-247;
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GI:21336157
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nucleic acid sequences of bladder tumour tissue Patent: WO 9954447-A 12 28-OCT-1999;
PERMIN (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)
LOCATION/Qualifiers
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                                  TTCGAAAACCTGCTGGTGCTGAGTCCTGTGTGGGGGCACCCCACACGACACCCCTCTTCCC
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Pred. No. 3.1e-212;
0; Mismatches 3;
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/db_xref="taxon:9606"
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Best Local Similarity 99.5%;
Matches 879; Conservative
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BCO27769 3139 bp mRNA linear ROD 07-AUG-2002
Mus musculus, clone MGC:38375 IMAGE:5345297, mRNA, complete cds.
BCO27769
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Gaithersburg, Maryland;
             TGGGACTCCTTGGGTATCAAGACCTATGCCACATCACACTGGGGCTAGGGAAGTAGGTGA
                                                  TGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTC
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                                                                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/clone_lib="NCI_CGAP_Mam6"
/note="Vector: pCMV-SPORT6"
208 .846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                             be found
                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 55 Row: d Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Pred. No. 2.1e-198;
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  Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
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/organism="Mus musculus"
/db_xref="taxon:10090"
/map="FVB/N"
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 GAGAGCAGGGCAGCAGCTGGCTAAGGAGTACGGCATGGACTTCTACGAAACAAGTGCCT
                                     GCACCAACCTCAACATTAAAGAGTCATTCACGCGTCTGACAGAGCTGGTGCTGCAGGCCC
                                                                                                               ATAGGAAGGAGCTGGAAGGCCTCCGGATGCGTGCCAGCAATGAGTTGGCACTGGCAGAGC
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/translation="MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVD
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SFTRLTELVLQAHRKELDGLRTCASNELALAELBEDEGKTEGPANSSKTCWC"
                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                Sprague-Dawley) (library: LAMBDA ZAPII)
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1 (bases 1 to 945)
Elferink,L.A. Anzai,K. and Scheller,R.H.
rabls, a novel low molecular weight GTP-binding specifically expressed in rat brain
J Biol. Chem. 267 (9), 5768-5775 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.7%; Score 577.6; DB 10; llarity 88.7%; Pred. No. 1e-137; Conservative 0; Mismatches 79;
                                                                                                                                                                         Location/Qualifiers
1. .945
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                                                                                                                                                                                                                                  /tissue_type="brain"
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                                                                                                                                                                                                              /strain="Sprague-Dawley/db_xref="taxon:10116"
                             adult bland
Rattus norvegicus
Bukaryota, Metazoa, Chordata,
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 LMW GTP-binding protein.
Rattus norvegicus (strain
adult brain cDNA to mRNA.
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/gene="RAB15"
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                       1754 GGCCAGGGACAGCAGTTTGCACAGCAGAGGGGAATGTAGCAACAGCAGGGCCTCCTAGGC
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Sprague-Dawley (clone LRB9) RAB15 mRNA, complete cds.
M83679 G1:206536
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         King, G.E., Meagher, M.J., Xu, J. and Secrist, H. Compositions and methods for the therapy and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                      2642 CTAGGGAAGTAGGTGATGCCAGCCCTCAAGTCTGTCTTCAGCCAGGGACTTGAGAAGTTA 2701
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0; Mismatches 3:
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CORIXA CORPORATION (US)
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Sequence 303 from Patent W00212328.
AX396088
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0194629-A 5329 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and thelic order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                           Baylor Plaza, Houston, TX 77030, USA
On Aug 9, 2002 this sequence version replaced gi:21723229.
                                                                                                                                                                                                                                 Chemistry: Dye-Terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 116551 bases at least Q40 consensus quality: 123470 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
                                                           Center: Baylor College of Medicine
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Center clone name: CH230-16122
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                                               COMMENT
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Station, C. Allen, H., Alsbrooks, S., Anin, A., Anguishoo, D., Anyallen, C., Allen, H., Alsbrooks, S., Anin, A., Anguishoo, D., Anyallen, C., Allen, H., Alsbrooks, S., Anin, A., Anguishoo, D., Anyale, M., Anguishoo, D., Anyale, M., Anguishoo, D., Anyale, M., Barata, Baden, H., Bandaranike, D., Barnstaed, M., Benahmed, F., Biswalo, D., Bandaranike, D., Barber M., Barnstaed, M., Benahmed, F., Biswalo, D., Bandaranike, D., Barber M., Barnstaed, M., Benahmed, F., Biswalo, D., Carter, K., Cavazos, I., Ceasar, H., Center, A., Carter, C., Chen, C., Coyel, M., Cree, D., Drown, M., Duval, B., Carter, C., Chen, C., Ding, Y., Chan, T., Chen, Z., Chon, T., Char, C., Chen, C., Ding, Y., Charger, M., Cree, D., Drown, M., Bugene, C., Bung, Y., Durbi, K., Duval, B., Eaves, K., Fernandez, S., Finly, M., Eugern, C., Dun, A., Durbin, K., Duval, B., Eaves, K., Fernandez, S., Finly, M., Flagg, N., Forbes, L., Poster, M., Poster, M., Capter, M., Gapter, M., Hanland, M., Hanll, C., Hamilton, C., Hamilton, C., Hanland, M., Hanland, M., Mandon, S.L., Modgeon, L., Jacop, H., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Jang, H., Johnson, B., Johnson, R., Marger, M., Mahladun, S.L., Handerson, M., Mandon, M., Ma
Rattus norvegicus clone CH230-16122, *** SEQUENCING IN PROGRESS A**, 70 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (pases 1 to 162495)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                AC096084.6 GI:22164942
HTG; HTGS_PHASE1.
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                                                                                                                                 Norway rat.
Rattus norvegicus
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| Db 125410 CCCTCCCCCAGTCCCTTCCGTGGAGGCCCGTGGAGGCCAGGGAGTCTGGGCTTTG 125354 Qy 761 CCCTGCTGCTGTCTCTCGTGTGATGACTATGAGTATCAGTAGCCACTACTCCCCT 820 | CCAGGCCACTTTCAGCTGCTCCTTCCGTGCATCGTGTTTTCTCTGCTTTTTCTCTT | 1300 CCCACTGTCCCTCATGGGCCTGCCCCCAGTGACCTGCGAAAGTGGAGCATC 1359 1360 CCCACTGTCCCTCATGGGCCTGCCCCCCAGTGACCTC 1 1 1 1 1 1 1 1 1 | |
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| 33443: gap of uni 34975: contig of 35075: gap of uni 37579: contig of 37679: gap of uni 39003: contig of 40564: contig of 40664: gap of uni 40664: gap of uni 40679: gap of uni 42079: gap of uni 43598: contig of 43598: contig of 4518: contig of 4518: contig of 47859: gap of uni 47859: contig of | of 1459 bp in I unknown length of 1365 bp in I unknown length of 1863 bp in I unknown length of 2811 bp in I unknown length of 2565 bp in I unknown length of 2182 bp in I unknown length of 2182 bp in I unknown length of 1149 bp in I unknown length of 2314 bp in I unknown length | 0826/ 70091: contig of 1825 pp in length 70092 70191 gap of unknown length 70192 70191: gap of unknown length 70192 7288 74787: contig of 2696 bp in length 7298 74782: contig of 1795 bp in length 74783 74883 74782: contig of 1795 bp in length 77248: contig of 2366 bp in length 77248: contig of 1936 bp in length 77349 77349 gap of unknown length 77349 79379: gap of unknown length 79379: gap of unknown length 83158: gap of unknown length 83159 83259 gap of unknown length 85364 85463: gap of unknown length 85363: contig of 2105 bp in length 85364 88527: contig of 3064 bp in length 8658 88627: contig of 1824 bp in length 86528 88627: contig of 1824 bp in length 86528 88627: contig of 1824 bp in length | Ouery Match Query Match 13.0%; Score 423.6; DB 2; Length 162495; Best Local Similarity 61.8%; Pred. No. 1.5e-97; Matches 1227; Conservative Oy 523 AGTCATTCACGCGTCTGACAGACTGGTGCTGCAGCCCATAGGAAGACCTGGAGGCC 582 |

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Query Match
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omplete cds.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                             TCC-----CCCAGAGTCCGTGGACAACAGGCCT----TAAACATGGCAAGAGGGCGG 124208
                                                                                                                                                                                                                                     Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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 AGAGCATTTCCTCAGACTCCCAGGCGGAGGACTGAGCCTAGCCTTCAGCAACCAAGGTTC
                                                                                                          CCCTGGGTAGAAACGCTTGGTGCTGTTCTCTTTTGGCCTTTTAAGACAAAGCGCTCATCTTG
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                                                     TCCTGGGACCCAAAGTTTATGGGAGAAGGCAAAGACTTCATGGGAAGAGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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Eukaryota; Metazoa; Chordata; '
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 2560)
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/product="Unknown (protein for MGC:6897)"
/protein_id="AAH13790.1"
/db_xref="G1:15489394"
/db_xref="G1:10="MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMYIDVDGIKVPTQJWDFRQDERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKADEEQKRQVGREQGQLAKEYGMDFYETSACFFSSFFS
                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam2"
                                                                                                                                                   Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 5 Row: i Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Genomescan gene prediction.
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                       ONA Sequencing by: Baylor College of Medicine Human Genome
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                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Library Arrayed by: The I.M.A.G.E.
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154. .660
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                                                                                                                         Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/db_xref="taxon:10090"
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Db 135389 AGTCCTTCACTCGACGAGCTGCTGCTGCAGGCCCACAGGAAAGAGCTGGATGGTC 135330
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38600. .46661
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/note="assembly_name:Contig11"
14856. .23382
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122783. .169668
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244802. 246147
/note="assembly_name:Contig6"
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note="assembly_name:Contig16"
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Best Local Similarity 61.29
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Mus musculus chromosome UNK clone RP23-246K11, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 257226)
McPherson, J. D. and Waterston, R. H.
The sequence of Mus musculus clone
551 GAGAGCAGGGCCAGCAGCTGGCTAAGGAGTACGGCATGGACTTCTACGAAACAAGTGCCT 610
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-trainator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 249197 bases at least 030
Consensus quality: 250905 bases at least 030
Consensus quality: 251159 bases at least 030
Insert size: 214000; agarose fp
Insert size: 25826; sum-of-contigs
Quality coverage: 9.36 in 020 bases; sum-of-contigs
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Center code: WUGSC
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s: gap of unknown length
c: contig of 9622 bp in length
s: gap of unknown length
c: contig of 8527 bp in length
c: gap of unknown length
c: contig of 15017 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mus musculus
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| Db 134265 GCGGGCTCCTAGAACCAGGGTTAGAGCAAGAGCAGAGGAGCTTCGCA 134218 Ov 1775 CAGCAGAGAGAAATATAGCAAAAGCAAGAGCACCTTCCTT | | 1835 AAGAAGACAFTCCTCAGACTCCCAGGCGGAGGACTCAGCCTAGCCT | QY 1895 GTTCTCCTGGGACCCAAAGTTTATGGGAGAAGGGCAAAGACTTCATGGGAAGAGAAGG 1954 | 1955.AAGGCCCTGGGTAGAAACGCTTGGTGCTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCAT 201 | OY 2015 CITGCCCTCTACCTCATAGGCTTGCCAACCACCACGCTGGGCTGC 2074 - H | Qy 2075 AGGGAAGAGCTCCTTCCTCAGAGTGCTATGTTCAGGAAGTTTCTTTAACCCCATATG 2134 | OY 2135 GCCCAAGAGTAGCTCGTAGGAGGCCCTTTAAAGACGGAACAAGTAATTAC 2185 | OY 2186 CAGTCTACTGGGGTTCCTGCCCACCGTCCCAAGGTGGGCGAAGCGAAGAGGGTCA 2245 | QY 2246 TTCTTAAGCCACATTAGCTGCACTGCGTGCAAAAAAAAAA | QY 2305TGAGTATTCATCAACTAAGAACCAAAATCCAGGGCACTCATATGTGAAGGATAAG 2359 | 2360 AACCTCACTTCCTTACTCCTCCAAAAAGAAGTGGGGAAAGAACCATCAA | OY 2418 CCTGACTTACCAAACCAGGAAACACAGGAGAGGGGGGCTCAGGACTTA 2467 | AX341683 | TION Sequence 1930 ION AX341683 N AX341683.1 G1 DS : | SOURCE Anuman. ORGANISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. | Jiang, Y. Composit | JOURNAL PATENT: WO 0196388-A 1930 20-DEC-2001; CORIXA CORPORATION (US) FEATURES Source 1313 | /organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 68 a 85 g 73 t 2 others |
|---|---|--|---|---|--|--|---|--|--|---|---|--|--|--|---|--|---|---|
| | OY 703 ACACGACACCCTTTCCCTCAGGAGCCCGTGGGCAGCAGGGGAGCCGGGGCTTTGCC 762 | QY 763 CIGCTGCTCTCGTGTGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCCTGC 822 | QY 823 CTGGCCCTGAGAGCGGCTCTGCTGTCATCTC-AAGCAGCCCCTGTCCCCAGCCCGTC-CA 880 | | QY 941 TGTGCCGCAAGCACTGTCTCACCATCCCGCACCACAGACACAGGCTGGAGTC 1000 | QY 1001 CAGGCCACTTTCAGCTGCTCCTTTCTCCGTGCATCGTGTCTTCTCTGCTTTTTTCTCTC 1060 | | AAACCCCGTCCCCCGTGTGTCCTGCTGTGCAGCTCGCTCTTTCCTTCC | 1181 ATCCAAGGGATGACCCAGGCTCGTGGGGAGGTTCCACCTTGGATCCAGGAAGACCC 134760 TITTCCTTCCTGATCTGCTTAGGAATGGACCAGGCTCTTGCATCCAGGAACGAATGGACCAAGGCTCTTGCCTCAGGAATGGAATGGACCAAGGCTCTTGCCCAGGAATGGAATGGACCAAGGAATGGACCAAGGAATGGAACAAGAATGAAATAGAAATGAAATGAAATAGAAATGAAATAGAAATGAAATAGAAAATAGAAATAGAAATAGAAATAGAAATAGAAATAG | 1241 TCCACCTGCTCGTGGTGGCCAAAGGCTACAGGGTGCTTCTTCCTCTTCCCCACCC | 1301 CCACTGTCCCTCATGTGCCATGGGCCTGCCCAGTGACCTGCGAAAGTGGAACATGG 1301 CCACTGTCCCTCATGTGCCATGGGCCTGCATGACTGACTG | OY 1361 AGGTAGGAGAAACAGCAACCGGGAGTCCTCGAGCCTGGGGCTGCCCTACCTCTACCC 1420 Db 134607 AGGTAGGAAGGAAACAGTACTAGGTGGCCTCAAGCCTGGACTGGCCTTTCTGCCTT 134550 | OY 1421 ATTCCCCGACCAGCAGCTTTGCCTTGCTTGGCTGCCTGCC | OY 1481 CTCAGAGGCAGGTGCTTCAGAGAAGGAAATGAGGGGTGGCAGGGATAAA 1534 | OY 1535 AAGTCACCTCCATTCTCTACCTCCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTC 1594 Db 134431 AAGTCACCTCTGTTCTCTACCTCCCATGCCTCTCTCCTCACTGGATTC 134383 | Qy 1595 CCAAATTTAAAGATGTGGACCAGTGGGTACTCCAGGGGCAAGGACAGCCTGGG 1654 | QY 1655 GTCAGTGACACTGTCAGGCCAACCATGCACAAAGGGGAGCATTTGGAAATGAAGG 1714 | Qy 1715 ACTAGCTCCTATGTATCAGGTTAAGAGCAAGGGGGGGGGG |

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ORIGIN
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ó 2884 TCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGG 2943 Gaps ; 0 9.4%; Score 307; DB 6; Length 313; 99.0%; Pred. No. 6.1e-68; tive 1; Mismatches 2; Indels Query Match
Best Local Similarity 99.0°
Matches 308; Conservative 3124 AACTTCGTGTA 3134 301 AACTICGIGID 311 à q ò qq δ qq g οy ò g δ

Search completed: November 17, 2002, 20:03:03 Job time : 6495 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                         November 17, 2002, 20:40:59 ; Search time 1956 Seconds (without alignments) 1755.339 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES * Sult Query No. Score Match Length DB ID Solution | 1 996 90.1 1091 12 BF1660330 BF536642 BF535642 BF535642 BF535642 BF535642 BF535642 BF635642 BF635642 BF648588 B1648588 B1648588 B1648588 B1648588 BF17816 BF17 | 858.5 77.7 796 12 BF966292 BF181167 BF181167 BF181167 BF181167 BF181167 BF181167 BF181167 BF181167 BF182001 BF1 | 26 649 58.7 385 1 27 5 589 53.3 956 1 29 554.5 50.2 714 1 30 551.5 49.9 644 1 31 547 49.5 678 1 32 545 49.3 678 9 34 545 49.3 678 9 36 545 49.3 676 9 37 545 49.3 885 1 40 545 49.3 886 9 41 545 49.3 886 9 42 545 49.3 886 9 43 545 49.3 886 9 44 545 49.3 887 1 44 545 49.3 887 1 45 545 49.3 887 1 46 545 49.3 887 1 47 545 49.3 887 1 48 545 49.3 887 1 49 545 49.3 887 1 | SULT 1 160330 CUS BF160330 CUS EINITION 601768601F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3987745 5', MRNA sequence. CESSION BF160330.1 GI:11040541 YWORDS MUS musculus BURCE house couse. ORGANISM Wus musculus BURATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MARMANIA; EUtheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. |
|--|--|--|--|---|
| Result No. | | 0 | 0 12020202020202020202020202020202020202 | RESULT 1 BF160330 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE |

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/strain="FVB/N"
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BF535642
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs -rémail.nih.gov
    Tissue Procurement: Gilbert Smith, Ph.D.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    http://image.llnl.gov
    blate: LLAM3195 row: b column: 02
    High quality sequence stop: 654.
    i. 1091
        /organism="Mus musculus"
        /strain="CzecH II"
        /db_xref="taxon:10090"
        /clone="InAGE:3997745"
        /c
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

320 c 317 g 157 t
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996.00
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Best Local Similarity:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musns.
E 1 (bases 1 to 932)
NIH-MGC http://mgc.nci.nih.gov/.
L Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jéffrey E. Green, M.D.
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http://image.llnl.gov
Plate: LLAM9525 row: m column: 09
High quality sequence stop; 685.
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/clone="IMAGE:4193456"
/clone="IMAGE:4193456"
/clone=line="ncream="taxon: cone_line="taxon: cone_
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providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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1 (bases 1 to 992)
1 (hases 1 to 992)
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Matches:
Conservative:
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Best Local Similarity:
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TITLE
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603277781F1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5317917 5',
mRNA sequence.
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/fdev_stage="10 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
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National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLMAN1806 row: a column: 22

High quality sequence start: 2

High quality sequence stop: 614.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                  IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                        AAGTGGGTCAGTGACGTGGATGAGTACGCTCCAGAAGGAGTCCAGAAGATCCTAATTGGG

    616
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BI648588.1 GI:15562824
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AUTHORS
TITLE
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COMMENT
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ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGlu-GluGluGlyLysPr
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/strain="FVB/N"
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/dev_stage="10 months, virgin, virgin, virgin, virgin, virgin, virgin, virgin, virgin, virgin
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            Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMM177 row: p column: 16
High quality sequence stop: 706.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM9320 row: f column: 22

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                   1. .902
/organism="Mus musculus"
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/clone=lib="NCI_CGAP_Mams"
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/dev_stage="7 months"
/lab_hsst="DH10B"
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mRNA sequence.
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Best Local Similarity:
Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 699)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng to CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can to the contact of the contac
                          uThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeuVa
70 TyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuValTyrAsp
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Plate: LLAM11734 row: b column: 13
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/clone=lib="NCI_CGAP_Mam3"
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/dev_stage="10 months"
/lab_host="DH10B"
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF966292 73-JAN-2001
602286692F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4375366 5',
     al., Nature Genetics
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Reference for transgenic model: Xu 22, 37-43 (1999)."
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Mismatches:
Indels:
                                                                                                    Length:
Matches:
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885.00
98.87%
97.18%
80.09%
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295
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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TITLE
JOURNAL
                                                                157
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                                                                                                                                                                           /organism="Homo sapiens"
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution information can
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: Linkl0040 row: h column: 23
High quality sequence stop: 663.
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BF181167 1100 bp mRNA linear EST 31-OCT-2000 601805830F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036759 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1100)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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I. .1100
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                                                          AsnIleLysGluSerPheThr-ArgLeuThrGluLeuValLeuGlnAlaHisArgLys--
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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BF181167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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Best Local Similarity:
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
55 a 152 c 183 g 116 t
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BF182001 GI:11060143
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Matches:
Conservative:
Mismatches:
Indels:

    616
    /organism="Mus musculus"

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
Glound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10334 row: f column: 06
High quality sequence stop: 616.
Location/Qualifiers
           IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                                                                LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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Tyssue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov.
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Locyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9312 row: h column: 09
High quality sequence stop: 772.

Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1121)
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                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="lib="NIH_MGC_49"
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/lab_host="nelanotic melanoma, bigh MDR (cell line)"
/lab_host="nelanoma, bigh MDR (cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG762967 814 bp mRNA linear EST 15-MAY-2001
602735022F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4860437 5',
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArC/CDCTD/DTP
Tissue Procurement: ArC/CDCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA177 row: 1 column: 06
High quality sequence stop: 629.
Location/Qualifiers
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National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; C
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BG974411 GI:14362048
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Context: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                   362
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GluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuVal
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Plate: LLAM10978 row: h column: 22  
High quality sequence stop: 647.  
Location/Qualifiers  
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/db_xref="taxon:10090"
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/clone=lib="NCI_CGAP_Mam4"
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/dev_stage="5 months"
/lab_host="DH10B"
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Friner: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lochar Hennighausen Ph.D., Chu-xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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/lab_host="DH10B"
/lab_host="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Norl; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
   NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666417 5' SW:RB15_RAT P35289 RAS-RELATED PROTEIN RAB-15. ;, mRNA
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Sciurognathi; Muridae; Murinae; Mus
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/ Organism="Mus musculus"
/ Organism="129.678L/60,FVB/N"
/ Ob_xref="124.xxxn:10090"
/ Clone="IMAGE:5318388"
/ Clone="IMAGE:5318388"
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/ Clossine_type="tumor, gross tissue"
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/ Alab_host="DH10B"
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/ Alab_host="DH10B"
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Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999).

2 2 2 2 4 9 195 t 2 others
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov e Column: 13 Plate: LLAMI1807 exquence stop: 777. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 ACAAGTGCCTGCACCAACCTTAATATAAAGAGTCCTTCACTCGTCTGACGGAGGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaGluLeuGluGluGluGluGlyLysProGluGlyProAlaAsnSerSerLysThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 IleGluValAspGlyIleLysValArgIleGlnIleTrpAspThrAlaGlyGlnGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 TyrGlnThrIleThrLysGlnTyrTyrArgArgAlaGlnGlyIlePheLeuValTyrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 ThrSerAlaCysThrAsnLeuAsnIleLysGluSerPheThrArgLeuThrGluLeuVal
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Mismatches:
Indels:
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1 (Dases 1 to 1767)

1 (Dases 1 to 1767)

1 (Mases 1 to 1767)

2 NIH-MCC http://mgc.nci.nih.gov/.

2 National Institutes of Health, Mammalian Gene Collection (MGC)

2 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapba-rdmail.nih.gov

3 Tissue Procurement: ArC

3 CON Library Preparation: Life Technologies, Inc.

3 CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

5 DNA Sequencing by: Agencourt Bioscience Corporation

5 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

5 High quality sequence start: 89

6 High quality sequence start: 89

7 High quality sequence start: 89

8 High quality sequence start: 89

8 Location/Qualifiers
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/clone="INAGE:54912"
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/note="Organ: eps; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Technologies."
                                                                                                                                                                                                                                                                               BM462147 1767 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6424626 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491242
121 AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 SerGluArgSerTyrGlnHisIleMetLysTrpValSerAspValAspGluTyrAlaPro 111
                                                                LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 others
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/db_xref="taxon:9606"
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AUTHORS
TITLE
JOURNAL
COMMENT
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BM462147
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Search completed: November 17, 2002, 22:05:03 Job time : 1962 secs

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1105
1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKFFGPANSSKTCWC 212
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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SPTREMBL_21:* •• Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_vertebrate:*
sp_unclassified:* sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:*
sp_plant:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_rodent:* sp_virus:* sp_human:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | Q91yw0 mus musculu | 09tys2 caenorhabdi | 015971 drosophila | Q8vcf6 mus musculu | 018338 drosophila | Q9h0t3 homo sapien | Q9dd03 mus musculu | Q9het4 aspergillus | 024466 arabidopsis | Q40218 lotus japon | Q40215 lotus japon | 09fjfl arabidopsis | Q94148 caenorhabdi | Q40219 lotus japon | Q8vwf9 nicotiana t | 040177 lycopersico |
|----------------|-----------------------------------|---|--|---|--|--|--|---|---|---|---|---|---|---|--|---|
| ΠD | Q91YW0 | Q9TYS2 | 015971 | QBVCF6 | 018338 | О9нотз | Q9DD03 | Q9HET4 | 024466 | 040218 | 040215 | Q9FJF1 | Q94148 | 040219 | Q8VWF9 | 040177 |
| DB | 11 | 2 | 5 | 11 | Ŋ | 4 | 11 | ٣ | 10 | 10 | 10 | 10 | 'n | 10 | 10 | 10 |
| Length | 168 | 211 | 204 | 207 | 207 | 200 | 202 | 206 | 216 | 214 | 216 | 216 | 201 | 215 | 216 | 216 |
| Query Match | 72.2 | 50.4 | 49.5 | 49.0 | 47.8 | 47.6 | 47.6 | 47.1 | 47.0 | 46.9 | 46.7 | 46.6 | 46.5 | 46.5 | 46.4 | 46.3 |
| Score | 798 | 557 | 546.5 | 541 | 528.5 | 526.5 | 526 | 521 | 519 | 518 | 515.5 | 515 | 514 | 513.5 | 513 | 512 |
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| | Query Score Match Length DB ID | Query Score Match Length DB ID 798 72.2 168 11 Q91XW0 | Query Score Match Length DB ID 798 72.2 168 11 Q91YW0 557 50.4 211 5 Q9TYS2 | Query Score Match Length DB ID 798 72.2 168 11 Q91XW0 557 50.4 211 5 Q9TXS2 546.5 49.5 204 5 015971 | Query Score Match Length DB ID 798 72.2 168 11 Q91XW0 557 50.4 211 5 Q9TXS2 546.5 49.5 204 5 O15971 541 49.0 207 11 Q8VCF6 | Query Score Match Length DB ID 798 72.2 168 11 Q91YW0 557 50.4 211 5 Q9TYS2 546.5 49.5 204 5 015971 541 49.0 207 11 Q8VCF6 528.5 47.8 207 5 018338 | Query Score Match Length DB ID 798 72.2 168 11 091xW0 557 50.4 211 5 091xS2 546.5 49.5 204 5 015971 541 49.0 207 11 08VCF6 528.5 47.6 200 4 09H0T3 | Query Score Match Length DB ID 798 72.2 557 50.4 21 509TXS2 546.5 49.5 204 5015971 528.5 47.8 207 501838 526.5 47.6 200 4 09H073 526.5 47.6 202 11 09H003 | Query Query 5core Match Length DB ID 798 72.2 557 50.4 211 5 091Y82 546.5 49.5 50.7 201597 51 49.0 528.5 47.8 50.4 207 50.8 50.8 526.5 47.6 50 4 51 47.6 50 4 51 47.6 50 4 50 4 51 47.6 50 4 526.5 47.6 50 4 526.7 47.6 50 4 526.7 47.6 527.8 47.6 528.5 47.6 529.8 47.6 520.2 11 521.0 4 521.0 4 521.0 4 521.0 4 | Ouery Score Match Length DB ID 798 72.2 168 11 Q91xW0 557 50.4 211 5 Q9TxS2 546.5 49.5 204 5 015971 528.5 47.8 207 11 Q8VCF6 528.5 47.6 200 4 Q9HOT3 526.5 47.6 200 1 Q9D03 526.47.6 202 11 Q9DD03 521 47.1 206 3 Q9HET4 519 47.0 216 10 Q24466 | Query Score Match Length DB ID 798 72.2 168 11 Q91xW0 557 50.4 211 5 Q9TxS2 546.5 49.5 204 5 O15971 541 49.0 207 11 Q8VCF6 528.5 47.8 207 5 O1838 526.5 47.6 200 4 Q9H0T3 526.5 47.6 202 11 Q9DD03 521 47.1 206 3 Q9HET4 519 46.9 214 10 Q40218 | Query Query 798 72.2 168 11 091xW0 557 50.4 211 5 091xW0 546.5 49.5 20.4 5 01597 548.5 47.2 20.4 5 01597 546.5 49.5 20.4 5 01597 546.5 47.8 207 5 01833 526.5 47.6 200 4 09H073 526.5 47.6 202 11 09H073 521 47.1 206 3 09HET4 519 47.0 216 10 040218 515 46.9 214 10 040218 515 46.7 216 10 040218 | Ouery Score Match Length DB ID 798 72.2 168 11 Q91YW0 557 50.4 211 5 Q9TYS2 546.5 49.5 204 5 015971 528.5 47.6 207 11 Q9VCF6 528.5 47.6 200 4 Q9HOT3 526.5 47.6 200 1 Q9DD03 526.5 47.6 202 11 Q9DD03 521 47.1 206 3 Q9HET4 519 47.0 216 10 Q40218 515.5 46.6 216 10 Q40215 515.5 46.6 216 10 Q9FyF1 | Query Score Match Length DB ID 798 72.2 168 11 Q91xW0 557 50.4 211 5 Q9TxS2 546.5 49.5 204 5 015971 528.5 47.8 207 11 Q8VCF6 528.5 47.6 200 4 Q9H0T3 526.5 47.6 202 11 Q9DD03 526.5 47.0 216 10 Q9DD13 526.5 47.1 206 3 Q9HET4 519 47.0 216 10 Q40218 515.5 46.7 216 10 Q40215 515.4 46.6 216 10 Q9FyF1 514 46.5 201 5 Q94148 | Query Query 798 72.2 168 10 557 50.4 211 501xW0 546.5 49.5 204 501597 528.5 47.6 207 10 207 528.5 47.6 207 1 200 40 207 528.5 47.6 202 11 204075 208 <t< td=""><td>Score Match Length DB ID 798 72.2 168 11 091 W0 557 50.4 211 5 09 T V2 54.4 49.5 20.4 5 015 971 526.5 47.6 200 4 09 H073 526.5 47.6 200 1 09 D D D D D D D D D D D D D D D D D D</td></t<> | Score Match Length DB ID 798 72.2 168 11 091 W0 557 50.4 211 5 09 T V2 54.4 49.5 20.4 5 015 971 526.5 47.6 200 4 09 H073 526.5 47.6 200 1 09 D D D D D D D D D D D D D D D D D D |

121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSAC 153

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1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIDVDGIKVRIQ

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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RABIO OR DRABIO OR GG17060.
Drosophila melanogaster (Fruit fly).
Bussyota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IMDTAGQERFRITTATYRGAMGIILVYDITHERSFENIKNWIRNIEEHAASDVERMIIG 120
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 211;
                                                                                                                                                                 MAY-2000 (TrEMBLrel. 13, Created)
-UNN-2002 (TrEMBLrel. 21, Last sequence update)
-UNN-2002 (TrEMBLrel. 21, Last annotation update)
-UNN-2002 (TrEMBLrel. 21, Last annotation update)
-Elegans RAB-8 protein (corresponding sequence D1037.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.4%; Score 557; DB 5; Length 21:
55.0%; Pred. No. 6.9e-39;
ive 42; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid D1037.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF106592; AAK21367.2; -.
SEQUENCE 211 AA; 24022 MW; B7609A91B6082DA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AA
                                                                                                                           211 AA
        PRT;
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
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01-JUN-2002 (
01-JUN-2002 (
C. elegans RA
RAB-8.
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SUGURNE PROPERTY.

RAMAINE NO. COLINGES E. R. A. L. S. W. BOSKINS R.A. GOCCYDE J.D.,
RAMAINE W.D., COLINGES E. S. L. L. S. W. BOSKINS R.A. GOCCYDE J.D.,
RAMAINE W.D., COLINGES E. S. L. L. S. W. BOLL K.A., EDSKINS R.A. GOCCYDE R.A. MARINE R.D. COLINGES E. S. C. L. S. W. AMAINE M.D. COLINGES E. S. C. C. SCHEEFE S. E. M. L. S. W. BERDINE R.A. COLINGES E. S. C. C. C. BOLCHARS E. S. M. AMAINE M. B. M. S. W. C. BOLCHARS E. S. M. AMAINE M. S. M. S. W. C. BOLCHARS E. S. M. AMAINE M. S. W. C. BOLCHARS E. S. M. AMAINE M. S. W. S. W. BOLCHARS E. S. M. BARDEN E. S. M. AMAINE M. S. W. BOLCHARS E. S. M. BARDEN E. S. M. AMAINE M. S. W. BOLCHARS E. S. M. BARDEN E. S. W. BERNER E. M. BOLCHARS E. S. W. BERNER E. S. W. M. BERNER E. S. W. BERNER E. S. M. M. BARTIS M. W. BAULD S. W. GORD E. G. OFFIELD H. W. BORD E. W. BURDER E. S. WELLS E. G. GOLD E. M. W. BURDER E. W. BOLL M. B. W. BOLL M. B. W. BOLL M. B. W. BOLL M. W. BOLL M. B. W. BOLL M. W. BOLL M. B. W. BOLL M. B. W. BOLL M. W. BOLL M. B. W. BOLL M. W. BURDER E. W. BOLL M. W. BLUDGOR E. W. BURDER E. W. BOLL M. W. BURDER E. W. BOLL M. W. BURDER E. W. BOLL M. W. BURDER E. W. BURDE
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181 SPOGSSHGVKITVEOOK 197

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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                          60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                  120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                          Length 204;
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Last annotation update)
oncogene (derived from cell line
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                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019990. AAH19990.1; -.
InterPro: IPR0013579; GTPase_Rab.
InterPro: IPR001230; Prenyl_site.
InterPro: IPR0010806; Ras_trnsfrmng.
InterPro: IPR002078; S1954_interact.
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA4_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoptoctain.
SEQUENCE 204 AA; 23336 MW; 4E058761C6854920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00294; PRENYLATION; UNKNOWN 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN 1.
SEQUENCE 207 AA; 23668 MW; AC89DC85588FB8F8 CRC64;
                                                                       Query Match 49.5%; Score 546.5; DB 5; Best Local Similarity 49.8%; Pred. No. 5e-38; Matches 105; Conservative 47; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA.
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SMART; SM00175; RAB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 RMRASNELALAELEEEE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Ranantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.-H.C., Blazej R.G., Channep M., Pfeiffer B.D.,
Randon R.C., Rogers Y.-H.C., Blazej R.G., Channep M., Pfeiffer B.D.,
Randon R.C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Randon R.C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Randew R.W., Basud A., Baxendale J., Baytaktarolul L., Beasley E.M.,
Beeson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ranchits K.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Randondon K.J., Boung L.E., Downes M., Dugan-Rochas S., Fleischmann W.,
Rab B.D., Delcher A., Dang Z., Mays A.D., Davies P.,
Randoldek A., Gong F., Gorrell J.H., Gu Z., Gelbart W. M., Glasser K.,
Alostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchun K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchun K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchun K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kulup D., Martis M.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchun K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kulup D.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchun K.A.,
Alali M., Kalush F., Karpen G. H., Ke Z., Kennison D.A.,
Berkulo G. Milshina N.V., Mobrary C., Morris J., Moshrefi A.,
Andrei B., McIntosh H., Mount S.M., Nolson D.K.,
Alazool M., Pittann G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Randert K., Remington K.A., Nixon K., Worter E., Wang K., Wang K., Wassarman D.A., Walshinson S., Wang S., Wang S., Wall J., Wang S., Yang C., Sander S., 
                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Perryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rab proteins of Drosophila melanogaster: novel members of the Rab-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
                                                                                                         Last sequence update)
Last annotation update)
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                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
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MEDLINE-97228579; PubMed-9074639;
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                                                                                                   01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                              01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05,
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FEBS Lett. 404:65-69(1997).
                                                                                                                                                  RAB8 protein (LD44762p).
RAB8 OR CG8287.
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Satoh A.K., Tokunaga F.
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RESULT 5
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InterPro; IPR003579; GTPase_Rab.
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A MEDLINE-21154917; PubMed=11230166;
A MISOTGE W., Weile B., Wellenreuther R., Gassenhuber J., Glassl S., Wiemann S., Weil B., Wellenreuther R., Bauersachs S., Blum H.,
A Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
A Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
A Wambutt R., Korn B., Klein M., Poustka A.;
"Towards a Catalog of Human Genes and Proteins: Sequencing and
T Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
Genome Res. 11:422-435(2001).
-: SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
R EMBL, AL136650; CAB665885.1;
-: RISSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                              1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewisz S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL, D84347; BAA21711.1; -.
EMBL, AR069671; AAL39816.1; -.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2
                                                                                                                                                                                                                                                                                                             Length 207;
                                                                                                                                                                                                                                                                                                                                        40; Indels
                                                                                                                                                                                                                                                          PROSITE; PS00675; SIGERANGE.

GTP-binding; Lipoprotein.

TOTAA; 23691 MW; BE9DE812C77DCF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 22.5 kDa protein.
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N
                                                                                                                                                                                                                                                PROSITE; PS00294; PRENYLATĪON; UNKNOWN_1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                             47.8%; Score 528.5; DB 5 53.8%; Pred. No. 1.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AA.
                                                                                                                                                                                                                                                                                                                                      41; Mismatches
                                                                                                                              InterPro; IPR0013579; GTPase_Rab.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_Lrnsfrang.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SNART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; Small_GTP? 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                     FlyBase; FBgn0015796; Rab8.
                                                                                                                                                                                                                                                                                                                                        100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                         HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMRASN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMEANN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKFZP564L1962.
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local 3
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Rawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Schriml L.M., Staubli F., Suzuki R., Desole G., Quackenbush J.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Usonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ra Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rachons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ra Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Lasachiashi V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; NUSI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Fûnctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; AK002303; BAB22000.1; -.
EMBL; BC027214; AAR17214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                        TIGRFAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMAS4_INPERACT_1; UNKNOWN_1.
GTP-binding; Hypothetical protein; Lipoprotein.
GTP-binding; Hypothetical protein; Tipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
0610007031Rik protein (RIKEN CDNA 0610007N03 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.6%; Score 526.5; DB 4
Best Local Similarity 55.8%; Pred. No. 2.3e-36;
Matches 96; Conservative 45; Mismatches 3C
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=KIDNEY;
MEDLINE=21085660; Pubmed=11217851;
Afinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                       PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
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us-09-817-198a-2.rspt

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ATRABB (GTPase ATRABB).

RABB OR F4P12_310.

RABB OR F4P12_310.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                 DTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                   65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 - BEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT 64
 3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW
                   EU Arabidopsis sequencing project;
Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY:
EMBL; U82434; AAB65088.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Bloecker H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Bischoff F., Palme K.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Lipoprotein.
SEQUENCE 216 AA; 23939 MW; 1648E45B29D4EEB6 CRC64;
                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF 162
                                                                                                                                                   PRINTS, PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMAS4_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.0%; Score 519; DB 10; 51.9%; Pred. No. 1.1e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AL132966; CAB67668.1; -.
HSSP, P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005205; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Conservative
                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                  O24466;
O24466;
O1-JAN-1998 (
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A Punt P.J., Seiboth B., Weenink X.O., van Zeijl C.M., Lenders M.,
A Konetschny C., Ram A.F., Montlin R., Kubicek C.P.,
A Van Den Hondel C.A.;
Tidentification and characterisation of a family of secretion related
Train and Grasse encoding genes from the filamentous fungus Aspergillus
Train injer: a putative SEC4 homologue is not essential for growth.";
This submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
BENEL, AJZTAS688, CAC17832.1;
-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
BR HSSP: PO5713; 3RAB.
InterPro: IPR001806; Ras_trnsfrmng.
BR InterPro: IPR001806; Ras_trnsfrmng.
                                                                                                                                                                                                                                                                                                                                                                                                                     61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                   1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.1%; Score 521; DB 3; Length 20
Best Local Similarity 60.6%; Pred. No. 6.8e-36;
Matches 97; Conservative 30; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                              GTP-binding; Lipoprotein. SEGUENCE 202 AA; 22770 MW; 5DF599432E228AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP-binding; Lipoprotein.
SEQUENCE 206 AA; 22823 MW; 501916B795CF8CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                             TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                              Query Match 47.6%; Score 526; DB 11; Best Local Similarity 54.1%; Pred. No. 2.5e-36; Matches 92; Conservative 45; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AA
                                           InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secretion related GTPase, (SrgA).
             MGD; MGI:1915578; 0610007N03Rik.
InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMG.
SMART; SM00175; RAB; 1.
                                                                                                                              PRINTS; PR00449; RASTRNSFRMNG.
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                                                                                                                                               SM00175; RAB; 1
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                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HET4
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Q9HET4
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Gaps

Indels

Length 216;

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MEDLINE=97231679; PubMed=9076991;
Borg S., Brandstrup B., Jensen T.J., Poulsen C.;
Identification of new protein species among 33 different small GTP-
binding proteins encoded by cDNAs from Lotos japonicus, and expression
of corresponding mRNAs in developing root nodules.";
Plant J. 11:237-250(1997).
- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR.2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Rab-type small GPP-binding protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudioctyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99087489; PubMed-9872454; Askamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23776 MW; 569926CCA8D1B489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
SEQUENCE 216 AA; 23776 MW; 569926CCA8D1B489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 515.5; DB 1
48.3%; Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 A--EPQTIQINQPDASASGGQAAQKSC 213
                                                                                                                                                                                                                                                                                                                               Interpro; IPR003579; GTPase_Rab.
Interpro; PR001080; Ras_trnsfrmng.
Interpro; IPR002078; Sig54_interact.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ASNELALAELEEEGKPEGPANSSKTC
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                            EMBL; 273944; CAA98172.1; -. HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                 SEQUENCE FROM N.A.
TISSUE=ROOT NODULES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                          NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-COLUMBIA;
  japonicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97231679; PubMed-9076991;
Borg S., Brandstrup B., Jensen T.J., Poulsen C.;
Identification of new protein species among 33 different small GTP-
indentification of new protein species among 33 different small GTP-
binding proteins encoded by CDNAs from Lotos japonicus, and expression
of corresponding mRNAs in developing root nodules.";
Plant J. 11:237-250(1997).
-- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
EMBL; Z73947; CAAA9175.1;
-- HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 -EEQKRQVGREQGQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 YDYLIKLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRVKLQIMDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 518; DB 10; Length 21
Pred. No. 1.3e-35;
8; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 AA; 23627 MW; 5E1A6E83505E50D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0231; small_GTP; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA
                                                                                                                                       214 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GLRMRASNELALAELEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 TLKINQDSAAGAGE-----AANKSSCC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1g54_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
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                                                                                                                                       PRT;
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SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.9%;
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01,
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                                                                                                                                       PRELIMINARY;
                                                                                                                                                                           01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                       192 TIKINQSDQ 200
  179 GLRMRASNE 187
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=34305;
                                                                                                                                                                                                                                                                             Lotus japonicus
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Q40215;
01-NOV-1996 (
01-NOV-1996 (
01-JUN-2002 (
RABBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
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Q40215
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201 AA;
                                              Matches 100;
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Q40219
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                                                                                                                                                                                                                                                                   AGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-124 FROM N.A.

Noned M.L., Staunton J.E., Kilgard M.P., Fergestad T., Jorgensen E., Hartweig E., Horvitz H.R., Meyer B.J., Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.

EMBL; U6033; AAC48200.1; --

EMBL; U60357; AAB16972.1; --
                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                 12 YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                     YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
 -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY
                                                                                                                                                                         Length 216;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;
Wamsley P., Bradshaw H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     GTP-binding; Lipoprotein.
SEQUENCE 216 AA; 23834 MW; E1370672F6EF3364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                      46.6%; Score 515; DB 10; I
47.6%; Pred. No. 2.3e-35;
tive 43; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00175; RAB; 1.
TIGREAMS; TIGR00231; small_GTR; 1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
                                                                                                                        PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              201 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   192 TIKISQTDQAAGA-----GQATQKSAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                            InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; S1954_interact.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003379; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR002078; Sig54_interact.
Interpro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                      PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                 InterPro; IPR003579; GTPase_Rab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00449; RASTRNSFRMNG.
          EMBL; AB015475; BAB08351.1; -. HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                               Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borg S., Brandstrup B., Jensen T.J., Poulsen C.; Identification of new protein species among 33 different small GTP-binding proteins encoded by cDNAs from Lotos japonicus, and expression of corresponding mRNAs in developing root nodules."; Plant J. 11.237-250(1997).

- I SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY. EMBL; Z73948; CAA98176.1; HSSP: P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Majnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae, Lotus.
NCBI_TaxID=34305,
                                                                                                                                                                                                                                                                        QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                             GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                        Gaps
                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT 64
                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                         Length 201;
                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23715 MW; E7912846E919D608 CRC64;
22712'MW; 2D205ABF751EBF1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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PROSITE; PSOG75; SIGMA54_INTERACT_1; UNKNOWN_1.
GTP-binding; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 513.5; DB 1/46.9%; Pred. No. 3.1e-35; iive 43; Mismatches 53
                                                Score 514; DB 5;
Pred. No. 2.5e-35;
                                                                                                48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LRMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | : | | : | | 172 AKMPDSTD----EQSRDTVNPVQPQRQSSSGGC 200
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InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR002078; Sig54_interact.
InterPro; IPR005225; Small_GTP.
Pfan; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SWART; SW00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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TISSUE-ROOT NODULES;
MEDLINE-97231679; PubMed-9076991;
                                                46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J; Lipoprotein
215 AA; 2371!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lotus japonicus.
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72 AGQERFRITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 - EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILLIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YDYLIKLLIGDSGVGKSCLLIRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT 64
                                                                                                                                                                                                                                                                                                                              RAB8-4 OR RAB8-2.
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae, euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          11)

SEQUENCE FROM N.A.

STRAIN-BRIGHT YELLOW 2;

STRAIN-BRIGHT YELLOW 2;

A TOTAINGTON N., Shimada K., Ito K., Yamamoto K.;

Lobinatelerization of Rab8 from tabacco BY-2 cell.";

Lobinited (JAN-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; AB079021; BAB84325.1;

REMBL; AB079021; BAB84323.1;

RICEPTO: IPR001806; Ras_trnsfrmng.

RICEPTO: IPR002078; Sig54_interact.

PRINTS; PR00419; RASTRNSFRWNG.

REMORY: SMO0175; RAS_1.

REMORY: SMO0175; RAS_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
46.4%; Score 513; DB 10; Length 21
Best Local Similarity 46.7%; Pred. No. 3.4e-35;
Matches 99; Conservative 44; Mismatches 53; Indels
                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ras-related protein RAB8-4 (Ras-related protein RAB8-2).
                                                                              178 EGLRMRASNELALAELEEEEGKPEGPANSSKTC 210
                                                                                                                192 TGIKIN------PQDKGSAGEAAQKSACC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: |: :| :1
192 AIRINQSDQAGTS------GQAAQKSSC 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        completed: November 17, 2002, 20:40:55
he : 83 secs
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                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                      Q8VWF9
                                                                                                                                                                          RESULT 15
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us-09-817-198a-2.rsp

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 17, 2002, 18:15:09; Search time 25 Seconds (without alignments) 351.719 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-817-198A-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKPEGPANSSKTCWC 212

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | rattı | P24407 homo sapien | disc | | disco | | 088386 homo sapien | рошо | rattn | | | Q39433 beta vulgar | | | P35281 rattus norv | P41924 yarrowia li | P20790 dictyosteli | | | | | Q39571 chlamydomon | | | | _ | O14462 candida alb | Q05737 zea mays (m | P07560 saccharomyc | | Q05974 lymnaea sta | | P11620 schizosacch |
|-----------|----------------|-------|--------------------|------------|------------|------------|------------|--------------------|------------|----------|------------|------------|--------------------|------------|------------|--------------------|--------------------|--------------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|
| SUMMARIES | ΩI | B15 | RAB8_HUMAN | RAB8_DISOM | RB13_HUMAN | RAO1_DISOM | RB10_CANFA | RB10_HUMAN | RB8B_HUMAN | RB8B_RAT | RAB8_MOUSE | YPT2_SCHPO | RAB1_BETVU | ARA3_ARATH | YPT2_VOLCA | RB10_RAT | RYL1_YARLI | SAS1_DICDI | YPT1_MAIZE | RIC1_ORYSA | SAS2_DICDI | RB35_HUMAN | YPT1_CHLRE | YPT1_PHYIN | ARA5_ARATH | YPT1_VOLCA | YPT1_NEUCR | SEC4_CANAL | YPT2_MAIZE | SEC4_YEAST | RB1B_RAT | RAB1_LYMST | RB1A_RAT | YPT1_SCHPO |
| | DB | ٦ | - | - | - | П | Н | ٦ | П | П | Н | П | ٦ | - | ٦ | - | - | - | Н | - | Н | 7 | - | ۲ | Н | - | - | - | -1 | Н | - | - | - | Н |
| | Length | 212 | 207 | 210 | 203 | 200 | 200 | 200 | 207 | 207 | 206 | 200 | 215 | 216 | 217 | 200 | 203 | 208 | 208 | 202 | 203 | 201 | 203 | 201 | 258 | 203 | 203 | 210 | 203 | 215 | 201 | 202 | 202 | 203 |
| | Query Match | | • | | | | | 8.0 | | | | | | | | | | | | | | • | | | | • | | • | 9. | | | 4. | 2.4 | 2.3 |
| dip. | Mai | 9 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | ₹ | ₹ | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 7 | 4 | 4 |
| | Score | 1077 | 545 | 539.5 | 532 | 531.5 | 530.5 | 530.5 | 528.5 | 528.5 | 526 | 510 | 509 | 208 | 505.5 | 502.5 | 502 | 483.5 | 483 | 480 | 479 | 477.5 | 477.5 | 477 | 476 | 475.5 | 475 | 473 | 470.5 | 470.5 | 469 | 469 | 468 | 467 |
| | Result No. | 7 | 0 | m | 4 | 2 | 9 | 7 | ω · | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 |

| P11476 homo sapien P22125 discopyge o | P01123 saccharomyc Q63482 rattus norv O9ulw5 homo sapien | P51156 rattus norv P25228 drosophila | 095716 homo sapien P11023 bos taurus | Q63942 rattus norv P05713 mus musculu | P20336 homo sapien |
|--|--|---|---|--|--------------------|
| RB1A_HUMAN RAB1_DISOM | YPT1_YEAST RB3C_RAT RB26 HUMAN | RB26_RAT RAB3_DROME | RB3D_HUMAN RB3A_BOVIN | RB3D_RAT RB3A_MOUSE | RB3A_HUMAN |
| | | | п п | | 1 |
| 205 | 206 219 190 | 190 | 219 219 | 219 220 | 220 |
| 42.3 | 41.3 | 41.0 | 40.2 | 40.0 39.9 | 39.7 |
| 467 | 456.5 455.5 454.5 | 452.5 | 444.5 | 442.5 | 439 |
| 34 35 | 36 37 38 | 39 40 | 41 | 44 | 45 |

ALIGNMENTS

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204 2
177 1
207 AA;
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Les 99; Conserv
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NP_BIND
DOMAIN
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RAB8_DISOM
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MEDLINE-31061765; Pubmed-2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                        61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                      61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                            121 NKADEEQKRQVGREQGQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                Gaps
                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94124602; PubMed-8294494;
Zahraoui A., Joberty G., Arpin M., Fontaine J.J., Hellio R.,
Tavitian A., Johovard D.;
"A small rab GTPase is distributed in cytoplasmic vesicles in non
polarized cells but colocalizes with the tight junction marker ZO-1
in polarized epithelial cells.";
J. Cell Blol. 124:101-115(1994).
                                                       1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoà; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91360267; PubMed-1886711; Minmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson R., Johnson K.J.; The MEL gene: a new member of the RAB/YPT class of RAS-related
                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
           Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Cell. Biol. 10:6578-6585(1990).-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
         Score 1077; DB 1;
Pred. No. 6.9e-80;
2; Mismatches 3;
                                                                                                                                                                                                                                                                           01-WAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Ras-related protein Rab-8 (Oncogene c-mel).
                                                                                                                                                                                                                                                                  207 AA
                                                                                                                                                                                       RMRASNELALAELEEEGKPEGPANSSKTCWC 212
                                                                                                                                                                                                  tch 97.5%;
al Similarity 97.6%;
207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 6:1347-1351(1991)
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human), and
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606, 9615;
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                                                                                                                                                                                                                                                                  RAB8_HUMAN
            Query Match
                        Local
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                                Matches
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EMBL outstation
                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IWDTAGOERYOTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
EFFECTOR REGION (BY SIMILARITY).
GERNAYL-GERANYL. (BY SIMILARITY).
LEGNSPQ -> WRATAP (IN REF. 2).
W; AA52DBF54A2CD056 CRC64;
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Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.3%; Score 545; DB 1; Length 207; 52.9%; Pred. No. 4.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
and the
Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Ras-related protein Rab-8 (ORA2).
Euscopyge ommata (Electric ray).
Eukaryota, Metazoa; Chordata; Craniata; Vertel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AA.
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45; Mismatches
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ISSUB-Electric lobe;
MEDLINE-91115900; PubMed-1899244;
Ngsee J.K., Elferink L.A., Scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
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TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                           MIM; 165040; -.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                   EMBL; X56741; CAA40065.1; --
EMBL; S53268; AAB196B1.1; --
EMBL; BC002977; AAH02977.1; --
EMBL; X56385; CAB56776.1; --
PIR; B45647; B49647.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23668 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
67
124
45
204
183
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RA01_DISOM
P22127;
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NP_BIND
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RAO1_DISOM
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NKCDMNEKRQVSKERGEKLAIDYGIKFLETSAKSSINVEEAFITLARDIMTKLNKKM--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
 family of ras-like GTP-binding proteins expressed in electromotor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94124602: PubMed-8294494;
Zahracui A., Joberty G., Arpin M., Fontaine J.J., Hellio R.,
Tavitian A., Louvard D.;
"A small rab Gress is distributed in cytoplasmic vesicles in non
polarized cells but colocalizes with the tight junction marker ZO-1
                                                                                                                                                                                                                                        InterPro,
Pfam: PF00071; Lac.
Pfam: PF004071; Lac.
PR00405; RASTRNs...
PR00405; RAB; 1.

( TIGREAMS; TIGR00231; small_GTP; 1.

W GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 15 22 GTP (BY SIMILARITY).
PT NP_BIND 63 67 GTP (BY SIMILARITY).

TIND 121 124 GTP (BY SIMILARITY).

37 45 EFFECTOR REGION (BY SIMILARITY).

CBRANYL-GERANYL (BY SIMILARITY).

CBRANYL-GERANYL (BY SIMILARITY).

TOT GERANYL (BY SIMILARITY).

PR 15 FFFECTOR REGION (BY SIMILARITY).

TOT GERANYL (BY SIMILARITY).

PR 15 FFFECTOR REGION (BY SIMILARITY).

TOT GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                      J. Biol. Chem. 266:2675-2680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                48.8%; Score 539.5; DB 1; Length 210; 47.4%; Pred. No. 1.2e-36; Live 56; Mismatches 45; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mono Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RMRASNELALAE-LEEEEGKPEGPANSSK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NENSLQEAVDKLKSPPKKPSQKKK 201
                                                                                                                                                                             PIR; B38625; B38625.
HSSP; P05713; 3RAB.
InterPro; IPR001379; GTPBSE_RAB.
InterPro; IPR001300; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR00525; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                  EMBL; M38391; AAA49232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ras-related protein Rab-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                         99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 99; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RB13_HUMAN
P51153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAB13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RB13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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E
                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: CYTOPLASMIC TIGHT JUNCTIONS OR ASSOCIATED WITH VESICLES SCATTERED THROUGHOUT THE CYTOPLASM IN CELLS LACKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                          -!- TISSUE SPECIFICITY: VARIETY OF EPITHELIA, INCLUDING INTESTINE,
                                                                                                                        Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD PARTICIPATE IN POLARIZED TRANSPORT, IN THE ASSEMBLY AND/OR THE ACTIVITY OF TIGHT JUNCTIONS OR ASSOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                KIDNEY, LIVER, AND OF ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GTP (BY SIMILARITY).
67 GTP (BY SIMILARITY).
(124 GTP (BY SIMILARITY).
45 EFFECTOR REGION (BY SIMILARITY)
200 GERANYL GERANYL (BY SIMILARITY)
22774 MW; 141621CB998178DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP-binding: Lipoprotein; Prenylation; Protein transport:
NP_BIND 15 22 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 532; DB 1; 47.6%; Pred. No. 4.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RMRASNELALAELEEEGKPEGPANSSKTC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003579; GTPBASE_RAb.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
polarized epithelial cells.";
Cell Biol. 124:101-115(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC000799; AAH00799.1;
HSSP; P01112; 1PLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X75593; CAA53266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:9762; RAB13.
MIM; 602672; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
67
124
45
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(Rel. 19, I
(Rel. 19, I
                                                                                                                                                                                                                                                                             TIGHT JUNCTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
37
200
203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                             SEQUENCE FROM N.A.
                                                                                                  TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991
01-AUG-1991
01-AUG-1991
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GTP-binding;
                                                                                                                                                                                                                                                                                                         NP_BIND
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAB10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RB10_HUMAN
                                                                                                                                                                                                                                                                                                                                                    LIPID
                               line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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                                                                                                                                                                this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                       SEQUENCE FROM N.A.
TISSUE-Electric lobe;
MEDLINE-91115900; PubMed-1899244;
MSGRE J.K., Elferink L.A., Scheller R.H.;
"A family of ras-like GTP-binding proteins expressed in electromotor
Ras-related protein ORA1.

Discopyge ommata (Electric ray).

Busaryota: Metazoa: Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea; Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Čhordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 41D38E3D760519C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%; Score 531.5; DB 1 56.4%; Pred. No. 4.9e-36; Live 44; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 AA
                                                                                                                                                                                                                                                                PIR; A38625; A38626.
HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
Pfam; PP00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
                                                                                                                                      J. Biol. Chem. 266:2675-2680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                           SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         22623 MW;
                                                                                                                                                                                                                                                      EMBL; M38390; AAA49230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ras-related protein Rab-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 56.4 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                          23
68
125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Cocker spaniel;
                                                                                                                                                                                                                                                                                                                                                                           16
64
122
200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                     NCBI_TaxID=7785;
                                                                                                                                                                                                                                                                                                                                                                 GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RB10_CANFA P24409;
                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
SEQUENCE
                                                                                                                            neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                           UP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
RB10_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAB10
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Pituitary;
SPECIES-Human; TISSUE-Pituitary;
SPECIES-20402571; PubMed-10931946;
Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
MEDLINE-91061765; PubMed-2123294;
Chavrier P., Vingron M., Sander C., Simons K., Zerial M.;
"Molecular cloning of YPT1/SEC4-related cDNAs from an epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606, 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein; Prenylation; Protein transport.

16 23 GTP (BY SIMILARITY).

12 125 GTP (BY SIMILARITY).

38 46 EFFECTOR REGION (BY SIMILARITY).

199 199 GERANYL-GERANYL (BY SIMILARITY).

200 200 GERANYL-GERANYL (BY SIMILARITY).

200 300 GERANYL-GERANYL (BY SIMILARITY).

30 A3; 22569 MW; 5D52B8E8E47D4362 CRC64;
                                                                                                                                                                                                             -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GNKCDMDDKRVVPKGKGEQIAREHGIRFFETSAKVNINIEKAFLTLAEDILR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 200;
                                                                                                                  MOI. Cell. Biol. 10:6578-6585(1990).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.0%; Score 530.5; DB 1;
55.8%; Pred. No. 5.9e-36;
iive 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEBLO-HUMAN STANDARD; PRT; 200 AA. 088386; Q9D7X6; 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUN-2002 (Rel. 38, Last annotation update) Ras_related protein Rab-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001579; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00071; ras; 1.
PRINTS; PR0049; RASTRINSFRNNG.
SMART; SM0175; RAB; 1.
TIGRRAMS; TIGRO0231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X56387; CAA39798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; D36364; D36364.
HSSP; P05713; 3RAB.
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200 AA;
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Query Match
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NP_BIND
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DOMAIN
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Matches
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X SPECIES—Mouse, STRAIN—C57BL/6J; TISSUE—Stomach;

X Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

X Arawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kosukawa T., Saito R.,

X Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

X Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Dromstein M.J., Bult C., Fletcher C., Fullita M., Maziballi M., Mombaerts P.,

A Urons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

X Wanshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nananana M., Wang K., Wang K., Wangi K., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.; "Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
                                                                                                                                                                                                                                Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Hakatashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiquchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Niomiya K., Iwayanagi T.;
"NEDO human cDNA sequenching project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                                                                                                                 Wong K., Hong W., Tang B.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zeng Q., Tan Y.H., Hong W.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF106681; AAD43034.1; -. EMBL; AF297660; AAG13413.1; -. EMBL; AK023223; BAB14474.1; -. EMBL; BC000896; AAH00896.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Human; TISSUE-Cervix;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                 SEQUENCE FROM N.A.
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60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen D., Guo J., Gahl W.A.;
"RAB GTPsses expressed in human melanoma cells.";
Biochim. Biochis. Acta 1355:1-6(1997).
--- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSATTER RELEASE (BY SIMILARITY).
--- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .9e-36;
es 29; Indels
                                                                                                                                                                                                                                                                                                        GTP-binding; Lipoprotein; Prenylation; Protein transport.
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TISSUE-Fetal brain;
Seki N., Selito T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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7F02B8E8E46EE1E8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.0%; Score 530.5;
55.8%; Pred. No. 5.9e
:ive 46; Mismatches
EMBL; AF035646; AAC29313.1; -.
EMBL; AK008725; BAB25858.1; -.
HSSP; P05713; 3RAB.
Genew; HGNC: 9759; RAB10.
MGD; MGI:105066; Rab10.
InterPro; IPR00359; GTPasse_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR001806; Ras_trnsfrmng.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                        PRINTS; PRO0449; RASTRINSFRMNG.
SMART; SM00175; RAB; 1.
TIGRPAMS; TIGR00231; small_GTP; 1.
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MEDLINE-97182150; PubMed-9030196;
                                                                                                                                                                                                                                                                                                                     23
28
28
28
46
199
200
106
N
22541 MW; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 96; Conserv
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RABS OR MEL.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Armstrong J., Thompson N., Squire J.H., Smith J., Hayes B., Solari algentification of a novel member of the Rab8 family from the rat basophilic leukaemia cell line, RBL.2H3.";
J. Cell Scl. 109:1265-1274(1996).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROPPRANSATTER RELEASE (BY SIMILARITY).
-!- TISSUE SPECIFICITY: HIGHEST LEVELS OF EXPRESSION IN THE SPLEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                           121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
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                                                                                                                                                                                                                                                         GTP-binding; Prenylation; Lipoprotein; Protein transport.

NP_BIND
63 67 GTP (BY SIMILARITY).

NP_BIND
121 124 GTP (BY SIMILARITY).

DOMAIN
37 45 EFFECTOR REGION (BY SIMILARITY).

LIPID
204 GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                          47.8%; Score 528.5; DB 1; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
                                                                                                                                                                                                                                                                                                                                   5960993C0F87F944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    47; Mismatches
                                                                                                                                                     Interpro; IPR003579; GTPase_Rab.
Interpro; IPR001230; Prenyl_site.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                    PRINTS; PR00449; RASTRNSFRANG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGR00231; Small_GTP; 1.
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                                                                                                      EMBL, AB038995; BAA92249.1; -. EMBL, BC020654, AAH20654.1; -. EMBL; U66624; AAC51199.1; -. HSSP; PO5713; 3RAB.
                                                                                                                                                                                                                                                                                                                                    23584 MW;
                                                                                                                                                                                                                                                                                                                                                                         54.0%;
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204 2
207 AA;
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P70550;
                                                                                                                                                                                                                                                                                                                       LIPID
SEQUENCE
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                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on ng as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKES-FTRLTELVLQAHRK 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFFECTOR REGION (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
4A41AB26BF9DCAF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91360267; PubMed-1886711;
Nimmo E.R., Sanders P.G., Padua R.A., Hughes D., Williamson
Johnson K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 6:1347-1351(1991).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
                                                                                                                                                                                                                                                     InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001300; Prenyl_site.
InterPro; IPR001200; Ras_trnsfrung.
InterPro; IPR001806; Ras_trnsfrung.
InterPro; IPR005225; Small_GTP.
Pfam; PF00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
TIGRFAMS; TIGREAMS; TIGREAMS; TIGREAMS; TIGREAMS; Lighter (Transport.)
GTP-binding; Prenylation; Lipoprotein; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 47.8%; Score 528.5; DB 1; Local Similarity 54.0%; Pred. No. 8.9e-36; hes 95; Conservative 47; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Ras related protein Rab-8 (Oncogene c-mel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 AA.
   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23603 MW;
                                                                                                                                                                                         EMBL; U53475; AAA99782.1; -. HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
45
204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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TIGRFAMS;
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Best Local (
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NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hengst L., Lehmeier T., Gallwitz D.; "Structural and functional analysis of ypt2, an essential ras-related gene in the fission yeast Schizosaccharomyces pombe encoding a Sec4
                                                                                                                                                                                                                                                                                         61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                     61 IWDTAGQERFRITTTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-11848401; PubMed-11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
                                                                                                                                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GFFECTOR REGION (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

49D832725D662942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fawell E., Hook S., Sweet D., Armstrong J.; "Novel YPT1-related genes from Schizosaccharomyces pombe."; Nucleic Acids Res. 18:4264-4264(1990).
                                                                                                                                                                                                          47.6%; Score 526; DB 1; Length 206; 56.4%; Pred. No. 1.4e-35;
                                                                                                                    GTP-binding; Prenylation; Lipoprotein; Protein transport;
                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                                                                                                                                                121 NKADEEOKROVGREOGOOLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                              41; Mismatches
                          MGD; MGI:96960; Mel.
InterPro; IPR003579; GTPsse_Rab.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001806; Rss_trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                          TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
MEDLINE-90269232; PubMed=2112089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-90332438; Pubmed=2115995;
                                                                                       RASTRNSFRMNG.
                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                        23557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homologue.";
9:1957-1962(1990).
         EMBL; S53270; AAB19682.1;
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ras-related protein ypt2.
                                                                                                                                                                                                                    Local Similarity 56.4
nes 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                      22
67
124
45
203
                                                                                      PRINTS; PR00449; RASTRN SMART; SM00175; RAB; 1
                                                                            Pfam; PF00071; ras; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4896;
                                                                                                                             Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                   YPT2_SCHPO
P17609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-972
                                                                                                          TIGRFAMS;
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                         NP_BIND
DOMAIN
                                                                                                                                                                                                           Query Match
                                                                                                                                       NP_BIND
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Matches
                                                                                                                                                                                                                                                                                                                                                                                           YPT2_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ADEEGKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KSYDYLIKLLIGDSGVGKSCLLLRFSEDSFTPSFITTIGIDFKIRTIELDGKRIKLQIW 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: THIS PROTEIN IS ESSENTIAL FOR CELL VIABILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:871'880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY. PROBABLE YEAST SEC4 HOMOLOG.
Chillingworth T., Churcher C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%; Score 510; DB 1; Length 200; 51.9%; Pred. No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP-binding; Lipoprotein; Prenylation; Protein transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2C658D153A290C30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR003579; GTPase_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X52469; CAA36707.1; -.
EMBL; X52864; CAA37045.1; -.
EMBL; 299262; CAB16405.1; -.
PIR; S10493; S10493.
PIR; S12790; S12790.
HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22755 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRAFFIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
68
125
46
199
200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
199
200
200 AA;
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184 ASNELALAELEEEGKPEGPANSSKTCWC 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 YDYLIKLLLIGDSGVGKSCLLLRFSDGSFTTSFITTIGIDFKIRTIELDGKRIKLQIWDT 71
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96307523; Pubmed-8680960;
Dallery E., Quief S., Ben Jilany K.E., Kerckaert J.-P., Hagege D.;
Dallery E., Quief S., Ben Jilany K.E., Kerckaert J.-P., Hagege D.;
"Molecular cloning and structural analysis of cDNAs that encode 3 amall GTP-binding proteins from sugar beet.";
C. R. Acad. Sci., III, Sci. Vie 319:91-97(1996).
-I. SIMILARITX: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AGQERFRIITTAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDNVNKILVGNKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.1%; Score 509; DB 1; 47.8%; Pred. No. 3.5e-34;
                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Ras-related protein RABIBV.
                                                                                                                                                          215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein; Prenylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003579; GTPase_Rab.
InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00071; ras; 1.
PROWAS; PROWAS; RASTENSFRNNG.
SMART; SMO0175; RAB; 1.
TIGRPAMS; TIGR00231; small_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z49152; CAA89021.1; -. HSSP; P05713; 3RAB.
                                                                                                                                                                                                                                                                   Beta vulgaris (Sugar beet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 1
212 2
213 2
215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                  183 RASNELA 189
                                                                               176 DAENEFS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3TP-binding;
                                                                                                                                                        RAB1_BETVU
Q39433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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NP_BIND
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA Salanoubat M., Lemcker, Rieger M., Ansorge W., Unseld M.,
RA Salanoubat M., Lemcker, Rieger H., Perez-Alonso M., Obermaler B.,
Beltmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaler B.,
Delseny M., Boutry M., Girvell L.A., Mache R., Puigdomench P.,
RA Delseny M., Boutry M., Artiquell L.A., Mache R., Puigdomench P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wurmbach E., Drzonek H., Erifle H., Jordan N., Bangert S.,
Wurmbach E., Drzonek H., Rarifle H., Jordan R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Ronrad A., Hornischer K., Rauer G., Loehnert T.-H., Nordsiek G.,
RA Navarro P., Collado C., Perez-Perez A., Otterwæelder B., Duchemin D.,
RA Mantro P., Callado C., Perez-Perez A., Otterwæelder B., Duchemin D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Masuy D.,
Androw T., Rizzo M., Walts A., Utterback T., Fullon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fullon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fullic C.Y., Shea T.P.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., Willte O., Venter J. C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Murakl A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Ra Sasamoto S., Kimura T., Idesawa K., Rakashima K., Kishida Y.,
Randade A., Yanada M., Tasuda S., Takeuchi C., Wada T.,
Randade M., Shinpo S., Takeuchi C., Wada T.,
Randade M., Masuda M., Tasuda S.) f the plant Arabidopsis
                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
115-JUN-2002 (Rel. 41, Last annotation update)
Ras-related protein ARA-3.
ARA-3 OR AT3G46060 OR F12M12_30.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNAs encoding small GTP-binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ., Hasegawa K., Watanabe Y., Uchimiya H., Ishizaki R.,
                                                                                                                                                                                                                           216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Various strains; TISSUE-Leaf;
MEDLINE-92084144; PubMed-1748311;
                                                                                                                                                                                                                       PRT;
190 AOPSITIKPADO----SGNOAAAKSACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D01025; BAA00830.1; -. EMBL; AL355775; CAB90933.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and analysis of
of Arabidopsis thaliana.";
Gene 108:259-264(1991).
                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           ARA3_ARATH
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24143 MW;
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Ras-related protein Rab-10.
                  EMBL; LO8128; AAA34251.1;
PIR; S36365; S36365.
HSSP; PO5713; 3RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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72
129
50
215
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                                                                                                                                                                                                                                                                                                                                                                                    217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                      Multigene family.
NP_BIND 20
NP_BIND 68
NP_BIND 126
DOMAIN 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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LIPID
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RB10_RAT
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                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fabry S., Jacobsen A., Huber H., Palme K., Schmitt R., "Structure, expression, and phylogenetic relationships of a family of ypt genes encoding small G-proteins in the green alga Volvox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                    54; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet. 24:229-240(1993).
INCTION: PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR
                                                                                                                                                                              TRAFFIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                Length 216;
                                                                                                                                                                                                                                                                                                                                                ; DB 1;
4.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Query Match

46.0%; Score 508; DB
Best Local Similarity 46.9%; Pred. No. 4.2e
Matches 100; Conservative 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ASNELALAE-----LEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LSDTDSRAEPATIKISOTDQAAGAGQATQKSAC 213
                                                 Interpro; IPR003579; GTPBSE_Rab.
Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR001806; Ras_trnsfrmng.
Pfam; PP00071; ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM00175; RAB; 1.
IIGRFAMS; TIGR00231; SMAll_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94037148; PubMed-8221932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP-binding protein yptV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                            216 AA;
                                  P05713; 3RAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Volvox carteri
                                                                                                                                                                              GTP-binding; INP_BIND 7 NP_BIND NP_BIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPT2_VOLCA
P36861;
                                                                                                                                                                                                                                                                                                              SEQUENCE
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 PIR; J
PIR; J
HSSP;
                                                                                                                                                                                                                                                                        LIPID
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YPT2_VOLCA
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-!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE RAB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-92210533; PubMed-1313420;
Elferink L.A., Anzai K., Scheller R.H.;
"Rabl5, a novel low molecular weight GTP-binding protein specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 AGQERFRIITSAYYRGAQGIILVYDITDEASFNNVRNWWRNIEQHASDNVNKILVGNKLD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKAD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMR 183
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 YDALIKLLLYGDSGVGKSCLLLRFTDDMFTSSFITTIGIDFKIKKVDVDGKLVKLQIMDT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GERCTOR REGION (PROBABLE).

GERANYL-GERANYL (BY SIMILARITY).

GERANYL-GERANYL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 217;
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J. Biol. Chem. 267:5768-5775(1992).
-!- FUNCTION: MAY BE INVOLVED IN VESICULAR TRAFFICKING AND NEUROTRANSMITTER RELEASE.
HSSP; P05713; 3RAB.
InterPro; IPR003579; GTPase_Rab.
InterPro; IPR003225; Small_GTP.
InterPro; IPR003225; Small_GTP.
InterPro; IPR00375; Small_GTP.
Ffam; PF00071; ras; 1.
Ffam; PF00071; ras; 1.
Fran; SM00175; RAB; 1.
SMART; SM0010; Small_GTPase; 1.
FIGRFAMS; TGR00231; Small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Indels
                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).
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(Rel. 28, Last sequence update)
(Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 505.5;
48.6%; Pred. No. 6.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ASNELALAE-LEEEEGKPEGPANSSKTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQLSAAQPVRLTSGSP-SPAQGKSCC 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RNKCDMDHKRVVPKGKGEQIAREHRIRFFETSAKANINIEKAFLTLPEDILR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GTP (BY SIMILARITY).
68 GTP (BY SIMILARITY).
125 GTP (BY SIMILARITY).
46 EFFECTOR REGION (BY SIMILARITY).
199 GERANYL-GERANYL (BY SIMILARITY).
200 GERANYL-GERANYL (BY SIMILARITY).
22858 MW; EFAF804FD4C3B6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 45.5%; Score 502.5; DB 1; Length 200; Best Local Similarity 53.5%; Pred. No. 1.1e-33; Matches 92; Conservative 47; Mismatches .32; Indels 1
                                                                                                                                                                                EMBL; M83677; AAA41991.1;

R EMBL; M83677; AAA41991.1;

R HSSP; P05713; 3RAB.

R InterPro; IPR003579; GTPase_Rab.

R InterPro; IPR005255; Small_GTP.

R Pfan; PR00417; Ras; 1.

R PRINTS; PR00449; RASTRNSFRMG.

R RIGKFMS; ITGR00231; Small_GTP; 1.

R TIGKFMS; ITGR00231; Premylation; Protein transport.

R TIGKFMS; ITGR00231; Small_GTP; 1.

R TIGK
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122
38
199
200
200 AA;
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LIPID
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Search completed: November 17, 2002, 20:39:12 Job time : 26 secs

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5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2002
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OM protein - protein search, using sw model

November 17, 2002, 20:35:44; Search time 43 Seconds Run on:

(without alignments)
473.965 Million cell updates/sec

US-09-817-198A-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC Title: Perfect score: Sequence:

212

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

STIMMARTES

| | Description | | ٦, | ⊣ . | | | | | | | GTP-binding protei | | GTPase AtRAB8 - Ar | hypothetical prote | Ω | | | | | GTP-binding protei | ~ | GTP-binding protei | | | | 0 | p. | | | | |
|-----------|---------------------|-----------|-----|----------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|------|----------|
| SUMMARIES | ID | TA 21 A 0 | | 133633 | 84964/ | B36364 | A49647 | A38625 | D36364 | B38625 | 178851 | B42148 | T45901 | T28971 | 833900 | T48378 | S12790 | T14565 | S57478 | JS0640 | T14405 | S57471 | 836365 | S57462 | S51495 | JC7589 | S57474 | A34716 | A38202 | m | S38740 · |
| | DB | ; , | 9 (| V | 7 | ~ | ~ | ~ | 7 | 7 | C | N | ~ | ~ | ~ | ~ | ~ | N | ~1 | ~ | ~ | 7 | ď | 7 | ~ | ~ | 7 | 7 | ď | ~ | ~ |
| | Length | 213 | 277 | 777 | 707 | 207 | 203 | 200 | 200 | 209 | 206 | 200 | 216 | 201 | 216 | 216 | 200 | 215 | 215 | 216 | 222 | 216 | 217 | 215 | 203 | 204 | 215 | 208 | 208 | 203 | 202 |
| • | * Query Match | 07 R | | 0.0 | 49.3 | 49.3 | 48.1 | 48.1 | 48.0 | 48.0 | 47.6 | 47.3 | 47.0 | 46.5 | 46.3 | 46.3 | 46.2 | 46.1 | 46.0 | 46.0 | 45.9 | 45.8 | 45.7 | 45.5 | 45.3 | 44.8 | 44.6 | 43.8 | 43.7 | 43.6 | 43.4 |
| | Score | 1077 | - C |) n | 04.1 | 545 | 532 | 531.5 | 530.5 | 530 | 526 | 522.5 | 519 | 514 | 512 | 512 | 510 | 509 | 508.5 | 508 | 507.5 | 206 | 505.5 | 502.5 | 501 | 495.5 | 492.5 | 483.5 | 483 | 482 | 480 |
| | Result No. | - | 4 (| 3 0 | η, | 4 | S | 9 | 7 | æ | o | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 |

181 181

RESULT 2

61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60

ŏ g δ 셤 Qγ q ŏ qq M73855 hypothetical protein D1037.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000 C;Accession: T33855 R;Ledwith, J.; Blewald, T. submitted to the EMBL Data Library, November 1998 A;Description: The sequence of C. elegans cosmid D1037.

| GTP-binding protei | ALIGNMENTS RESULT 1 F42148 GTP-binding protein rabl5 - rat C:Species: Rattus norvegious (Norway rat) C:Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 02-Feb-2001 | C;Accession: F42148 R;Elferink, L.A.; Anzai, K.; Scheller, R.H. T;Elferink, L.A.; Anzai, K.; Scheller, R.H. J. Biol. Chem. 267, 5768-5775, 1992 A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically express A;Reference number: A42148; MUID:92210533; PMID:1313420 A;Accession: F42148 | A;Molecule type: mRNÅ A;Rosidues: 1-212 <elf> A;Cross-references: GB:M3579; NID:g206536; PIDN:AAA41995.1; PID:g206537 C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine F;9-124,Pomain: translation elongation factor Tu homology <etu> F;9-124,Pomain: translation alongation factor Tu homology <etu> F;121-124,Region: nucleotide-binding motif A (P-loop) F;121-124,Region: GTP-binding NKXD motif F;210,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted</etu></etu></elf> | 1077; DB 2; Length 212; No. 9.2e-79; Smatches 3; Indels 0; Gaps 0; |
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| B34716 572515 772488 7724105 7724105 772533 772533 772533 771243 77183 714391 714391 714391 714391 714391 714391 | ALIGN protein rab15 - rat Rattus norvegicus (Norway rat) Sep-1993 #sequence_revision 30 | eller, R. 992 cular wei :92210533 | A; Molecule type: mRNA A; Residues: 1-212 <elfs A; Cross-references: GB:M83679; NID:920655 C; Superfanily: ras transforming protein; C; Keywords: GTP binding; lipoprotein; nuc F; 9-124/Domain: translation elongation fe F: 15-22/Region: nucleotide-binding motif F; 121-124/Region: GTP-binding NKXD motif F; 210, 212/Binding site: geranyl-geranyl (</elfs | Score 1077; Pred. No. 9.2 2; Mismatches |
| 10100000000000 | at (NO) | Sch 11 01e | ng proproproproproproproproproproproproprop | 8 86 96 96 |
| 2002 2003 2003 2003 2003 2005 2005 2005 | ol5 - rat gicus (N | 148; M | M83679 isformil ; lipo ition e ide-bi inding | 97.5%; 97.6%; vative |
| 44444444444444444444444444444444444444 | tein rab us norve | 2148 .; Anzai 267, 576 a novel ber: A42 2148 | mRNA 12 <elf> ces: GB: ras tran binding transla nucleot n: GTP-k</elf> | tch 97. al Similarity 97. 207; Conservative |
| 479 471.5 477.5 477.5 477.4 477.5 477.5 477.5 477.5 477.5 470.5 470.5 469 | ing prois: Rattu | ion: F4 nk, L.A Chem. rab15, nce numl ion: F45 | Molecule type: n Residues: 1-212 Cross-references: Superfamily: ras Keywords: GTP bi 79-124/Domain: tr 115-22/Region: n 121-124/Region: | Query Match Best Local Similarity Matches 207; Conser |
| 01000000000000000000000000000000000000 | RESULT 1 F42148 GTP-binding protein rabl5 C;Species: Rattus norvegic C;Date: 30-Sep-1993 #seque | C; Accession: F4218 R; Elferink, L.A.; Anz J. Biol. Chem. 267, 5 A; Title: rabl5, a nov A; Reference number: A A; Accession: F42148 A; Status: prelimhary | A;Molecule type: mRNA A;Rossidues: 1.212 (ELF> A;Cross-references: GB:16;Superfamily: ras tran C;Superfamily: ras tran C;Keywords: GTP binding F;9-124/Pomain: transla F;15-22/Region: nucleot F;121-124/Region: GTP-b F;210,212/Binding site: | Query Match Best Local Matches 20 |

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Richardoui, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Lou J. Cell Biol. 124, 101-115, 1994
A; Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized c A; Reference number: A49647; MUID:94124602; PMID:8294494
A; Status: prellainary
A; Molecule type: mRNA
A; Residues: 1-203 < ZAHS
A; Residues: 1-203 < ZAHS
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A; Molecule type: mRNA
A; Molecule type: mole
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C;Species: Canis lupus familiaris (dog)
C;Species: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
C;Accession: B36564; S15604
R;Chavrier, p.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell line.
A;Reference number: A36364; MUID:91061765; PMID:2123294
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C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Feb-2001
C;Accession: A49647
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A;Title: A small rab GrPase is distributed in cytoplasmic vesicles in non polarized cell A;Reference number: A49647; MUID:94124602; PMID:8294494
A;Accession: B49647
A;Status: nucleic acid sequence not shown
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binding; P-loop;
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A;Gene: CESP:D1037.4
A;Gene: CESP:D1037.4
A;Map position: 1
A;Introns: 10/3; 62/2; 82/3; 181/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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A/Residues: 1-207 <2AH>
A/Residues: 1-207 <2AH>
A/Residues: 1-207 <2AH>
A/Cross-references: EMBL-X56741; NID:9452317; PIDN:CAA40065.1; PID:9452318
R.Joberty, G.; Tavitian, A.; Zahraoui, A.
R.Joberty, G.; Tavitian, A.; Zahraoui, A.
FEBS Lett. 330, 323-328, 1993
A/Title: Isoperparjation of Rab proteins possessing a C-terminal Caax motif.
A/Reference number: $36817; MUID:93387463; PMID:8375503
A/Accession: $36817
A/Accession: $36817
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A/Accession: $175-186
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A;Experimental source: strain Bristol N2; clone D1037
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Jan-2001
C;Accession: B49647; S36817
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ive 45; Mismatches 43; Indels
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50.6%; Score 559; DB 2;
Best Local Similarity 55.3%; Pred. No. 2.1e-37;
Matches 105; Conservative 42; Mismatches 39
                     A;Reference number: 221424
A;Accession: T33855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-224 <LED>
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mes 99; Conservative
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    C; Accession: D36364; S15601
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A; Residues: 1-209 <NGS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Discopyge ommata
C.Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C.Accession: A38625
R.Accession: A38625
A.Title: A family of ras-like GTP-binding proteins expressed in electromotor neurons.
A.Reference number: A38625; MUD:91115900; PMID:1899244
A.Accession: A38625
A.Status: preliminary
A.Molecule type: manAA
A.Residues: 1-200 cMGS
A.Status: 1-200 cMGS
A.Cross-references: GB:M38390; NID:9213114; PIDN:AAA49230.1; PID:9213115
C.Superfamily: ras transforming protein; translation elongation factor Tu homology
C.Sepwords: GTP binding; membrane trafficking; nucleotide binding; P-loop
F:10-125/Domain: translation elongation factor Tu homology cFIU-125/Domain: GTP-binding motif A (P-loop)
F:152-125/Region: GTP-binding NKXD motif
F:152-154/Region: GTP-binding SAK/L motif
                                                                                                  Asp, Ser) #sta
      P-100p;
    nucleotide binding;
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GTP-binding protein rab10 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                  61 QIWDTAGQERFHTITTSYYRGAMGIMLVYDITNAKSFENISKWLRNIDEHANEDVERMLL 120
                                                                                                                                                                                                                                                                                                                61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                            NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                         1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                   1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 200;
                                                                                                  Thr, Thr,
predicted
                                                                                                                                                         Length 203;
                        公型
                                                                                                                                                                                               43; Indels
      membrane trafficking;
C; Keywords: GTP binding; lipoprotein; membrane construction factor Tu homology F: 15-22/ADomain: translation elongation factor Tu homology F: 15-124/Region: nucleotide-binding motif A (P-loop) F: 121-124/Region: GTP-binding NKXD motif F: 151-153/Region: GTP-binding SAK/L motif F: 151, 22, 40, 121, 122, 124, 151/Binding site: Mg-GTP (Lys, Thr, F; 200/Binding site: farnesyl (Cys) (covalent) #status prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ommata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.1%; Score 531.5; DB 2;
56.4%; Pred. No. 2.8e-35;
Live 44; Mismatches 30;
                                                                                                                                                         ; DB 2;
2.6e-35;

    electric ray (Discopyge

                                                                                                                                                       48.1%; Score 532; DE
47.6%; Pred. No. 2.6e
ive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRRSGN-----GNKP--PSTDLKTC 192
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mes 97; Conserv
                                                                                                                                                                         Best Local Similarity
Matches 100; Conserv
                                                                                                                                                           Query Match
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Cross-references: GB:M38391
C;Superfamily: ras transforming protein; translation elongation factor Tu homology C;Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loo F;9-124/Domain: translation elongation factor Tu homology <ETU>F;15-22/Region: nucleotide-binding motif A (P-loop)
F;121-14/Region: GTP-binding NKXD motif F;150-152/Region: GTP-binding SAK/L motif F;150-152/Region: GTP-binding CAS)
                                                                                                                                                                                                                                                                                                Tu homology
binding; P-loo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Discopyge ommata
C; Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C; Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 02-Feb-2001
C; Accession: B38625
B; Mysee, J. K.; Elferink, L.A.; Scheller, R.H.
J. Biol. Chem. 266, 2675-2680, 1991
A; Title: A family of ras-like GTP-binding proteins expressed in electromotor neurons. A; Reference number: A38625; MUID:91115900; PMID:1899244
A; Accession: B38625
A; Status: preliminary
R;Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. cell. Biol. 10, 6578-6585, 1990
A. Title: Molecular cloning of YPTI/SEC4-related cDNAs from an epithelial cell line.
A;Reference number: A36364; MUID:91061765; PMID:2123294
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                                                                                                                              A Accession: D36364
A Status: preliminary
A Holocule type: mRNA
A, Residues: 1-200 < CHA>
A; Residues: 1-200 < CHA>
A; Residues: 1-200 < CHA>
A; Cross-references: GB:X56387; NID:9914; PIDN:CAA39798.1; PID:9915
C; Superfamily: ras transforming protein; translation elongation factor Tu holocotics: GTP binding; lipoprotein; membrane trafficking; nucleotide bind F;10-125/Domain: translation elongation factor Tu homology < ETU>
F;16-23/Region: GTP-binding motif A (P-loop)
F;122-125/Region: GTP-binding SMX/L motif F;152-154/Region: GTP-binding SMX/L motif F;152-154/Region: GTP-binding SMX/L motif F;152-154/Region: GTP-binding setail (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IWDTAGQERFRTITTAXYRGAMGIMKVYDITNEKSFDNIKNWIRNIEBHASSDVERMILG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
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GTP-binding protein ora2 - electric ray (Discopyge ommata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 530.5; DB 2;
Pred. No. 3.3e-35;
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llarity 47.4%; Pred. No. 3.9e-35;
Conservative 56; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Mismatches
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Nitternate names: protein F4P12.300
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
C; Accession: T45901
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M. Submitted to the Protein Sequence Database, January 2000
A; Reference number: 223016
A; Reference number: 223016
A; Recession: T45901
A; Status: preliminary
A; Mocession: T45901
A; Status: preliminary
A; Mossidues: 1-216 < BLO>
A; Cross-references: EMBL:AL132966
A; Experimental source: cultivar Columbia; BAC clone F4P12
C; Genetics:
A; Map position: 3
A; Introns: 25/1, 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A; Note: F4P12.310
C; Superfamily: ras transforming protein; translation elongation factor Tu homology < F; 16-131/Domain: translation elongation factor Tu homology < ETU>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                           72 AGQERFRITITAYYRGAMGILLVYDVTDESSFNNIRNWIRNIEQHASDSVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQA-----HRKELE 178
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                                                                                                                               64
                                                                                           1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDT
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                                Indels
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R;Wammaley, P.; Bradshaw, H.
submitted to the EMBL Data Library, January 1997
A;Bescription: The sequence of C. elegans cosmid T23H2.
A;Reference number: Z20549
A;Accession: T28971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.0%; Score 519; DB 2; L. Best Local Similarity 51.9%; Pred. No. 3e-34; Matches 98; Conservative 42; Mismatches 43;
   Pred. No. 1.5e-34;
                             46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T45901
GTPase AtRAB8 - Arabidopsis thaliana
55.2%;
   Best Local Similarity 55.2
Matches 95; Conservative
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BH2148
GF2148
GF2148
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C;Date: 30-Sep-1993 #sequence_revision: 8.H.
J. Biol. Chem. 267, 5768-5775, 1992
J. Biol. Chem. 267, 5768-5775, 1992
A;Title: rabl; a novel low molecular weight GTP-binding protein specifically expressed A;Reference number: A42148; MUID:92210533; PMID:1313420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MEL.
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Reywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine
F;9-124/Domain: translation elongation factor Tu homology <ETU>
F;15-22/Region: nucleotide-binding motif A (P-loop)
F;121-124/Region: GTP-binding NIXD motif
F;151-153/Region: GTP-binding SAK/L motif
F;203/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: mRNA

A. Residues: 1-200 <ELF>

A. Cross-references: GBB.M83677

S. Superfamily: ras transforming protein; translation elongation factor Tu homology

C. Keywords: GTP binding, lipoprotein; nucleotide binding; P-loop; prenylated cysteine

F;10-125/Domain: translation elongation factor Tu homology <ETU>

F;10-213/Region: nucleotide-binding macif A (P-loop)

F;122-125/Region: GTP-binding NKXD motif

F;152-154/Region: GTP-binding SAK/L motif

F;199,200/Binding site: geranyl-geranyl (Cys) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                              К.Ч.
                                                                                                                                                                                                                                          GTP-binding protein MEL - mouse
N;Alternate names: gene MEL protein
C;Species: Mus Sp. (mouse)
C;Decies: Mus Sp. (mouse)
C;C;Decies: Mus Sp. (mouse)
C;Accession: 178851
R;Nimmo, E.R.; Sanders, P.G.; Padua, R.A.; Hughes, D.; Williamson, R.; Johnson, Oncogene 6, 1347-1351, 1991
A;Title: The MEL gene: a new member of the RAB/YPT class of RAS-related genes. A;Reference number: 158355; MUD:91360267; PMID:1886711
A;Accession: 178851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-206 <RES>
A;Cross-references: GB:S53270; NID:g234747; PIDN:AAB19682.1; PID:g234748
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.6%; Score 526; DB 2; 56.4%; Pred. No. 7.9e-35; tive 41; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 522.5;
                                                                 RMRASNELALAE-LEEEEGKPEGPANSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.38;
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Best Local Similarity 56.43
Matches 93; Conservative
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                             181
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Arabidopsis thaliana

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T48378
GTP-binding protein-like
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C; Species: Lycopersicon esculentum (tomato)
C; Accession: S33900; J02233
R; Fleming, A.J.; Mandel, T.; Roth, I.; Kuhlemeier, C.
R; Fleming, A.J.; Mandel, T.; Roth, I.; Kuhlemeier, C.
R; Fleming, A.J.; Mandel, T.; Roth, I.; Kuhlemeier, C.
R; Fleming, A.J.; Mandel, T.; Roth, I.; Kuhlemeier, C.
R; Fleming, B. Satterns of gene expression in the tomato shoot apical meristem.
A; Reference number: S33899; MUID:93222691; PMID:8467223
A; Accession: S33900
A; Molecule type: mRNA
A; Residues: 1-216 cFLL>
A; Cross-references: GB:X69980; NID:g313028; PIDN:CAA49600.1; PID:g313029
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: ras transforming protein; translation elongation factor Tu homology
C; Keywords: GTP binding; membrane protein; nucleotide binding; P-loop
F; 16-131/Region: uncleotide-binding metif A (P-loop)
F; 122-29/Region: GTP-binding NKXD motif
F; 159-161/Region: GTP-binding SAK/L motif
                                                                                                                                                                            A,Gene: CESP:T23H2.5
A,Map position: 1
A.Introns: 43/1; 147/2; 173/3
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
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                       A;Cross-references: EMBL:U80033; PIDN:AAC48200.1; GSPDB:GN00019; CESP:T23H2.5
A;Experimental source: strain Bristol N2; clone T23H2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GNKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| || :| ||:|::|:::|::|| ||:|| ||:| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.5%; Score 514; DB 2; Length 20 Best Local Similarity 46.9%; Pred. No. 7e-34; Matches 100; Conservative 48; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 LRMRASNELALAELEEEGKPEGPANSSKTCWC 212
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EPQSIRINQSDQAGTA 204
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A; Residues: 1-201 <WAM>
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Grecies: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 02-Feb-2001
C; Accession: S12790; S10493; T39214
R; Haubruck, H.; Engelke, U.; Mertins, P.; Gallwitz, D.
EMBO 7 9, 1957-1962, 1990
A; Title: Structural and functional analysis of ypt2, an essential ras-related gene in A; Reference number: S12790; MUID:90269232; PMID:2112089
A; Accession: S12790
A; Molecule type: DNA
A; Residues: 1-200 <AHD>
A; Cross-references: EMBL: X52469; NID:95143; PIDN:CAA36707.1; PID:95144
R; Fawall, E.; Hook, S.; Sweet, D.; Armstrong, J.
Nucleic Acids Res. 18, 4264, 1990
A; Title: Novel YPT1-related genes from Schizosaccharomyces pombe.
A; Reference number: S10492; MUID:90332438; PMID:2115995
A; Accession: S10492; MUID:90332438; PMID:2115995
A; Accession: S10493
A; Residues: 1-200 <FAW>
A; Residu
                                                                                                                                                                                                            Mewes, H.W.; Rudd, S.; Lemcke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Map position: 5
A;Introns: 25/1; 49/2; 83/1; 105/1; 137/3; 158/3; 189/3
A;Note: F12E4.300
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
F;16-131/Domain: translation elongation factor Tu homology <ETU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
N.Alternate names: protein F12E4.300
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Sacession: T48378
R.Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, March 2000
A.Reference number: 224492
A.Reference number: 24492
A.Reference number: 24492
A.Residues: 1-216 <BEV>
A.Residues: 1-216 <BEV>
A.Residues: 1-216 <BEV>
C.Genetics: cultivar Columbia; BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AGQERFRITTAYYRGAMGILLVYDVTDESSFNNIRNWAKNIEQHASDNVNKILVGNKAD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 -EEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF-----TRLTELVLQAHRK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YDYLIKLLLIGDSGVGKSCLLLRFSDDFFTTSFITTIGIDFKIRTVELDGKRIKLQIMDT 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 512; DB 2;
Pred. No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T39214
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
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Best Local Similarity
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A:Residues: 1-200 <MCD>
A:Cross-references: EMBL:299262; PIDN:CAB16405.1; GSPDB:GN00066; SPDB:SPAC9E9.07c
A:Cross-references: Exain 972h-; cosmid c9E9
C:Genetics:
A:Gene: ypt2
A:A pap position: 1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Reywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;
F:10-125/Domain: translation elongation factor Tu homology <FTU>
F:10-125/Region: GTP-binding mctif A (P-loop)
F:122-125/Region: GTP-binding NXXD motif
F:152-125/Region: GTP-binding SAK/L motif
F:152-154/Region: GTP-binding site: geranyl-geranyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 ADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match

46.2%; Score 510; DB 2; Length 200;
Best Local Similarity 51.9%; Pred. No. 1.4e-33;
Matches 97; Conservative 39; Mismatches 43; Indels
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176 DAENEFS 182
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Title: Perfect score:

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Scoring table:

Minimum DB Maximum DB

Searched:

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Sequence 7, Appli
Sequence 819, App
Sequence 885, App
Sequence 896, App
Sequence 836, App
Sequence 4, App
Sequence 4, Appli
Sequence 529, Appli
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Sequence 235, App
Sequence 901, App
Sequence 3393, Ap
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Patent No. US20020146758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
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Mismatches:
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US-09-817-198A-1
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LENGTH: 3257
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-Q=/cgn2_1/USPTO_spool/USO9817198/runat_13112002_135207_7068/app_query.fasta_1.391
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-MAXLEN-200000000 -USER-SSO9817198_GCGN_1_1_20_Grunat_13112002_135207_7068
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NGG_SCORES-0 -WAIT -LONGLOG
-DEV_INMEOUT-120 -WARR_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP-6
-FGAPEXT=7 -YGAPOP-10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 91, Appl
Sequence 631, App
Sequence 9, Appli
                                                                                                                                                                                November 17, 2002, 20:42:04; Search time 51 Seconds (without alignments) 1536.011 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PUBMW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
                              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                 - nucleic search, using frame_plus_p2n model
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US-09-925-302-91
US-09-925-300-631
US-09-794-257-9
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database :

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No. Result

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                                                                MetalaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly
                              JETUCRAT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 91
LENGTH: 1274
  US-09-817-198A-2 (1-212) x US-09-817-198A-1 (1-3257)
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LOCATION: (1268)
OTHER INFORMATION: n equals a,t,g, or
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Patent No. US20020044941A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,9,
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LOCATION: (1264)
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FEATURE:
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                                                                                                                                                                                              APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TILE REPERBNCE: PA101
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrp 211
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Matches:
Conservative:
Mismatches:
Indels:
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; Patent No. US20020151681A1
; GENERAL INFORMATION:
                      534.50
66.38%
43.40%
48.37%
                                     Percent Similarity:
Best Local Similarity:
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Patent No. US2002009804A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 33705, 2324, 27423, 32700, 32712, No. US20020009804A1e1
TITLE OF INVENTION: Human G-proteins
FILE REFERENCE: 35800/230285
CURRENT FILICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
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Mismatches:
Indels:
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Matches:
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                                                                                                                 NAME/KEY: misc feature
LOCATION: (5)
OTHER INFORMATION: n equals a,t,g, or
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-013-12 NUMBER OF SEQ ID NOS: 1890 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                              1.84e-57
530.50
82.56%
55.81%
48.01%
                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                      Best Local Similarity:
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                                                    SEQ ID NO 631
LENGTH: 1537
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US-09-794-257-7

Sequence 7, Application US/09794257

Sequence 7, Application US/09794257

Sequence 7, Application US/09794257

Sequence 7, Application US/090481

GENERAL INFORMATION: 3270200008804A1e1

TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804A1e1

TITLE OF INVENTION: Human G-Proteins

TITLE OF INVENTION: Human G-Proteins

FILE REFERENCE: 35800/20285

CURRENT APPLICATION NUMBER: US/09/794,257

CURRENT FILING DATE: 2001-02-27

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AAGACCTGCTCTGTTCCGCTTCTCAGAGGACGCCTTCAACACCACCTTCATCTCCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AsnLysAlaAspGluGluGluLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
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Mismatches:
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                                                                                                                                                                                           Length:
Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 624
                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                           9.02e-58
528.50
80.68%
53.98%
                                                                                                TYPE: DNA ORGANISM: homo sapiens
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ORGANISM: homo sapiens
                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                           Alignment Scores:
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                                                                                                                                     US-09-794-257-9
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APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Born, Jeffrey
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REPERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2001-04-14
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                                                   1161
95
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                                                   Length:
Matches:
Conservative:
Mismatches:
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 879
LENGTH: 2497
TYPE: DNA
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                                                 2.2e-57
528.50
80.68%
53.98%
47.83%
         ; LOCATION: (18)...(641)
US-09-794-257-7
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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NAME/KEY: CDS
                                         Alignment Scores:
Pred. No.:
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Sequence 885, Application US/09834975

Sequence 885 Application US/09834975

Fatent No. US20020110815A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MAI-016B

CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
FRICH FILING DATE: 2000-04-14
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 885
                                                           Ö
                                                              or
                           NAME/KEY: misc_feature
LOCATION: (1)...(2497)
COTHER INFORMATION: n = A,T,C
US-09-834-975-879
                                                                                                                6.62e-57
528.50
80.68%
53.98%
47.83%
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
Query Match:
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US-09-834-975-896
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APPLICANT: BOLT, Andrew
APPLICANT: BOLT, Andrew
APPLICANT: BOLT, Andrew
APPLICANT: BOLT, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
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                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
                                                                        Ö
                                             NAME/KEY: misc_feature

CATION: (1)...(2497)

CTHER INFORMATION: n = A,T,C or

US-09-834-975-885
                                                                                                                  6.62e-57
528.50
80.68%
53.98%
47.83%
            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                          Alignment Scores:
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LENGTH:
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APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CONRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
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                                                                                                                                                                                                                                       Length:
Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 894 LENGTH: 2497
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Patent No. US20020110815A1
GENERAL INFORMATION:
                                                                                                                                                          Ö
                                                                                                                                  ; LOCATION: (1)...(2497)
; OTHER INFORMATION: n = A,T,C or
US-09-834-975-894
                                                                                                                                                                                                                                     6.62e-57
528.50
80.68%
53.98%
                                                                                                                 NAME/KEY: misc_feature
                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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gAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysProGluGlyPr 203
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                               Length:
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                              Gaps:
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                                                                                                                             ; ORGANISM: Arabidopsis thaliana US-09-938-842A-836
                                                                                                                                                                              1.51e-56
519.00
71.64%
50.75%
                                                                                                                                                                                                                      Best Local Similarity:
Query Match:
                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                      Alignment Scores:
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                                                                                                                     TYPE: DNA
                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                     NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 896
LENGTH: 2497
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Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong
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                                                                                                                 , LUCATION: (1)...(2497); OTHER INFORMATION: n = A,T,C
US-09-834-975-896
                                                                                                                                                                                      6.62e-57
528.50
80.68%
53.98%
          PRIOR FILING DATE: 2000-04-14
                                                                                    ORGANISM: Homo sapiens
                                                                                                             NAME/KEY: misc_feature LOCATION: (1)...(2497)
                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                          Alignment Scores:
                                                                           TYPE: DNA
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366 CAGTGGCTGCAGGAGATTGACCGCTATGCCAGCGAGAACGTCAATAAGCTCCTGGTGGGG 425
                                                     140
                                                                                                                           141 LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
                                                                                                                                                             486 GACTCTCTGGGCATCCCCTTCTTGGAGGGGGCGCCAAGAATGCCAACAATGTCGAGCAG 545
                                                                                                                                                                                                  161 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu 180
                                                                                                                                                                                                                           591 GGAGCAGCCTCTGGGGGGGGGGGCGATCTCTCAAGATCGACAGCACCCCTGTAAAGCCG 650
                                                                                    426 AACAAGAGCGACCTCACCAACAAGAAGGTGGTGGACAACACCCACAGGCAAGGAGTTTGCA 485
                                                                                                                                                                                                                                                                           181 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlyLysPro 200
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                                                   AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
FRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-26
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96
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 529, Application US/09770445 Patent No. US20020023281A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Tampaka, Joshua G.
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477.50
65.57%
45.28%
43.21%
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Kricker, Maja
Slader, Ted
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Allen, Keith
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LENGTH: 881
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925
91
42
64
5
                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATIOR SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
         COLLEY, Neil C.
Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-817-198A-2 (1-212) x US-09-967-736-4 (1-925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF-0367 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 925 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.18e-51
478.50
65.84%
45.05%
43.30%
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CLONE: 2514506
Lal, Preeti
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                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                USA
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                                                                                                                                                                                                    ZIP: 94304
                                                                                                                                                           STATE: CA
                                                                                                                                                                              COUNTRY:
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{\tt AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet~100}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AACAAGTGTGATCTCACATCACAGAAAGTTGTATCCACTGAGACAGCTAAGGCTTTCGCT
                                                                                                                    IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
                                                                                                                                                                                            LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
APPLICANT: Gane Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR PLING DATE: 2000-11-02
PRIOR PLING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
PRIOR PLING DATE: 2001-05-15
                                                                                    US-09-817-198A-2 (1-212) x US-09-938-842A-832 (1-609)
 Conservative:
                  Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
FILING DATE: 2001-06-13
APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1461, Application US/09917800A patent No. US20020119462A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 SerPheThrArgLeuThrGluLeuVal 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 GCTTTCATGGCCATGACTGCTGCAATC 507
71.018
49.708
42.358
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APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
                  Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-917-800A-1461
     Percent Similarity:
                                     Query Match:
DB:
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APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: AND WARD AND
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PLILNG DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
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   60 ATGAATCCTGAGTACGACTATCTTTTCAAGCTCCTGCTTATCGGGGGATTCTGGCGTAGGC 119
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| AACAAGTCTGATCTTACTGAAAACAGAGCCATTCCTTATGAAACTGCCAAGGCTTTTGCC
                                                                                                                              41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln
                                                                                                                                                      101 LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly
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                                                          21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr
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Matches:
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ORGANISM: Arabidopsis thaliana
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468.00
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SEQ ID NO 832
LENGTH: 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLysGlu 142
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                                                                                                                                                                                                                                                                                                                               43 ValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIleTrp
                                                                                                                                                                                                                                                                                                                                                                                        23 CysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIleGly
                                                                                                                                              OTHER INFORMATION: Genbank Accession No. US20020119462A1 U37099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 ThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGlu 178
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                                                                                                                                                                                                    585
79
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Mismatches:
Indels:
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Matches:
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                 60/303,459
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Batta, Sajeev
Baughn, Mariah R.
TITLE OF INVENTION: RAS PROTEINS
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Lal, Preeti
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Patent No. US20020146770A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentin Ver. 2.1
LENGTH: 585
                                                                                                                                                                                                   1.15e-47
448.00
69.89%
44.89%
                                                                                                                ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                       Alignment Scores:
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                                                                                                    TYPE: DNA
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84 IlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLysTrpVal 103
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Matches:
Conservative:
                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0168-1 CIP TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         6.2
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Gaps:
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                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 6.1/MS-DOS CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/051,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/766,551
FILING DATE: DECEMBER 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: CENTONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                            FILING DATE: 15-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 10:
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429.00
68.48%
44.57%
38.82%
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                         COMPUTER READABLE FORM
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                                                                             CITY: Palo Alto
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                                                                                                                                  ZIP: 94304
                                                                                                                    COUNTRY:
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                                                                                                STATE:
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No.:
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Command line parameters:
-MODEL=frame+p2n.model.-DEV=x1h
-MODEL=frame+p2n.model.-DEV=x1h
-Q=/Cgn2_1/USFTQ_spool/USO9817198/runat_13112002_135206_7022/app_query.fasta_1.391
-Q=/Cgn2_1/USFTQ_spool/USO9817198/runat_13112002_135206_7022/app_query.fasta_1.391
-DB=N.Geneseq_101002 -OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=b1ts -STRAT=1 -END=-1 -MATRIX=b1osun62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MN=0 -ALIGN=15
-USER=USO9817199_@CGN_1_1125_@runat_13112002_135206_7022 -NCPU=6 -ICPU=3
-NO_XLEXY -NO_MANP -LARGEOFERY -REG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -YGAPOP=6 -FGAPOP=6 -FGAPOFT=7
                                                                                                                                                                                                                                                                                           November 17, 2002, 20:38:44; Search time 255 Seconds (without alignments) 1872.250 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA201A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA201B.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                         - nucleic search, using frame_plus_p2n model
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| SUMMARIES | ID | AAS2705 | 581 | AAS27472 | 770 | 3916 | 4 1 | AAF.180/2 | 010 | 4010 | 588 | 519 | AAH17889 | 145 | 518 | 996 | 987 | 88 | AAS60893 | 80 | 378 | 003 | AAH13912 | 2 0 | AAC34347 | 448 | 3842 | 801 | 368 | 4920 | 278 | 723 | 166 | 77.44 | AA193456 | 200 | 9 0 | ABN98761 | 26 | 1405 | 33398 | 8397 | 000 | 3520 | |
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ALIGNMENTS

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AAS27053;
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We encoding novel signal transc
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CDNA encoding novel signal transduction pathway protein, Seg ID 88.

Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; anti-inflammatory; anti-inflammatory; andi-inflammatory; andi-inflammatory; andi-inflammatory; andi-inflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease;

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Reproductive system; gastrointestinal; liver disorder; AIDS; ss; XX mocguired immune deficiency syndrome.  
XX
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PR 25-SEP-2000; 2000US-0234997.

PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-023534.

PR 29-SEP-2000; 2000US-023534.

PR 29-SEP-2000; 2000US-0235334.

PR 29-SEP-2000; 2000US-0235327.

PR 29-SEP-2000; 2000US-0235387.

PR 29-SEP-2000; 2000US-0235393.

PR 20-CCT-2000; 2000US-02341785.

PR 20-CCT-2000; 2000US-0241826.

PR 20-CCT-2000; 2000US-0246521.

PR 20-CCT-2000; 2000US-024921.

PR 20-CCT-2000; 2000US-0251999.

PR 20-CCT-2000; 2000US-0251999.

PR 20-CCT-2000; 2000US-02

AsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeuAla

121

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The invention relates to novel isolated polypeptides (I), and discontinuous proteins (II). (II) and the antibody to (I) are useful for disponsing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant relactions and graft versus host diseases, infectious diseases (e.g. hepatitis (), bleeding disorders, infelammatory conditions, organ transplant relacted disorders (sickle cell anaemia), myeloproliferative other blood-related disorders (sickle cell anaemia), myeloproliferative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal abnormalities (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of trecalls, to induce tumour proliferation in pathologies eg eg acquired immune deficiency syndrome (AIDS). AAS26976-AAS2780 represent novel signal transduction cynthemial sequences and PCR primers of the invention.
                                                                                                                                                                                                                    polypeptides useful for diagnosing, treating, preventing and/or using disorders related to the proteins, including cancers, immune
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 88; 880pp; English.
                                                                                                                                                                                                                                                                         disorders and neuronal disorders
                                                                                                 Ruben SM;
                                                (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678.
                                                                                                 Barash SC,
                                                                                                                                               WPI; 2001-465460/50
                                                                                                                                                                      P-PSDB; AAU17136
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MetAlaLysGlnTyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyValGly 21 LysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThr 2021 212 0 0 0 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: US-09-817-198A-2 (1-212) x AAS27053 (1-2021) 6.03e-118 1105.00 100.00% 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: 81 Score: à 셤 ò

41 IleGlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGln 임 δ

IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg 61 201 g g δ

AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet 100 81 261 ò g

321

LysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGly 120 101 381 ò

Whuman; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
w uniconvulsant; osteopathic; antiartic; immunosuppressant; cardiant;
Immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
w hypotensive; dermatological: immunosuppressive; antidiabetic;
w antiviral; antibacterial; antifungal; antitheumatic; antithyroid;
w antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
neurodegenerative disorder; osteoarthritis; graft vs host disease;
m enrodegenerative disorder; proliferative disorder; hypertension;
neurodegenerative disorder; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
alleryy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive; ss. 500 160 560 180 620 ArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGluGluGluGluGlUGlyLysPro 200 SerPheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeu LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu Human ORFX ORF1368 polynucleotide sequence SEQ ID NO:2735. BP. AAC75813 standard; cDNA; 1666 08-FEB-2001 (first entry) 501 199 141 161 181 AAC75813 RESULT g ŏ g Qγ q ŏ g ŏ g

99US-0127607. 99US-0127636. 99US-0127728. 31-MAR-2000; 2000WO-US08621. WO200058473-A2. Homo sapiens. 31-MAR-1999; 02-APR-1999; 05-OCT-2000.

2000US-0540763 (CURA-) CURAGEN CORP. 30-MAR-2000; 05-APR-1999;

40

9

80

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disordenerodegenerative disorders and cardiovascular disease P-PSDB; AAB41604.

Σ

Shimkets RA,

WPI; 2000-602362/57.

Claim 5; Page 1978-1979; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397 which represent the human ORFX open reading frames 1 to 3161. The ORFX

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sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; noctropic; neuroprotective; costeopathic; antiparkinsonian; noctropic; neuroprotective; costeopathic; anticonvulsant; thrombolytic; cosquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, enurodegenerative disorders, osteoarthritis, praft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus carptematosus, severe combined immunodeficiency (SCID), AIDS, viral, becterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concernant hemoglophuria, antiinflammatory disease; to enhance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt AlaGlnGlyIlePheLeuValTyrAspIleSerStuArgSerTyrGlnHisIleMet~100}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                        Sequence 1666 BP; 333 A; 529 C; 461 G; 341 T; 2 other;
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Mismatches:
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chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                                                                                                                                antiinflammatory; anti-HIV; antibacterial; antiinflammatory cancer; immune system disorder; rhemmatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                  cDNA encoding novel signal transduction pathway protein, Seq ID 507
                                                                                                                                      Neuroprotective; cytostatic; dermatological; immunosuppressive;
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2000US-0209467.
2000US-0214886.
                                                     AAS27472 standard; cDNA; 566
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17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
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LysGluLeuGluGlyLeuArgMetArgAlaSerAsnGluLeuAlaLeuAlaGluLeuGlu 194

571 AACCTCAACATTAAAGAGTCATTCACGCGTCTGACAGAGCTGGTGCTGCAGGCCCATAGG

DP GY

195 GluGluGluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrpCys 212

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2000US-0241221.
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20000S-0250130.
20000S-0250391.
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2000US-0254097.
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10 - DEC - 2000;
05 - DEC - 2000;
06 - DEC - 2000;
06 - DEC - 2000;
08 - DEC - 2000;
11 - DEC - 2000;
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Rosen CA, Barash SC, Ruben (HUMA-) HUMAN GENOME SCI INC.

WPI; 2001-465460/50. P-PSDB; AAU17555.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders -

Claim 1; SEQ ID No 507; 880pp; English

The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune system clisorders (e.g. congenital and acquired immunodeficiencies, autoimmune fisorders (e.g. theumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and chisorders, primary haematopoletic disorders, hyperproliferative disorders, primary haematopoletic disorders, hyperproliferative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders; (e.g. arrhythmia), respiratory disorders, (arrhators of disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of the invention in pathologies e.g. acquired immune deficiency syndrome (Alds) AAS26976-AAS27860 represent novel signal transduction conting sequences and PCR primers of the invention.

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                                                                                                             AlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMet
                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 34594
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2000US-0614150.
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              discloses genomic DNA sequences (ABL16176-ABL3051Í), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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polypeptides of the invention have homology to known proteins, thereby cylving an insight into their probable biological activities, thenceby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; inculding cytokine, cell proliferation or cell administration activities; stem cell growth activity; mannedulatory activity; tissue growth activity; mannedulatory activity; tissue growth activity; chemotatic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incliens and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, burnerial and dingal madelian to immune disorders. Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuropithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides cytokine; cell proliferation; cell differentiation; growth factor; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer antifungal; vulnerary; antiulcer; ss. Claim 1; Page 805; 1963pp; English. Liu C, Drmanac RT; 2000US-0496914. 2000US-0560875. 05-FEB-2001; 2001WO-US03800. WPI; 2001-457740/49. P-PSDB; ABB11916. (HYSE-) HYSEQ INC. WO200157188-A2. Homo sapiens. 03-FEB-2000; 27-APR-2000; 09-AUG-2001 Tang YT,

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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding novel human polypeptide of the invention.
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cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
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Mismatches:
Indels:
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                                                                          Sequence 1986 BP; 519 A; 545 C;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-C ABP4322B) and to cDNAs encoding them (ABD54131-ABD56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical comprision additionally relates to to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen solynucleotides against human ovarian antigen of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and catating, prognosing or preventing various ovary and/or breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, calsorders, infertility, disorders of pregnancy, anovulation, calsorders, infertility, disorders of pregnancy, anovulation, calsorders, infertility, disorders, and dysmenorrhoea), endocrine calsorders, infertility, disorders, e.g., congenital and acquired the cast of disorders, infertiling sequence of the conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired conditions (e.g., anaemia), articlorated disorders, neutrological disorders, gastrointestinal disorders, and urinary system disorders. Ovarian antigen polypeptides and conditions cativity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which collaborates and an antigen of the prepare antibodies caseful in disease diagnosis, drug targeting and phenotyping. The present collaboration of individuals and individuals and individuals and phenotyping of the presents of the pres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 290; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                                       07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSDB; ABP41333
                                                                                                                                                             WO200200677-A1.
                                                                                                             Homo sapiens.
                                                                                                                                                                                                                  03-JAN-2002.
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2411
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                Matches:
Conservative:
Mismatches:
Indels:
        Length:
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                                                                         US-09-817-198A-2 (1-212) x ABQ54410 (1-2411)
        2.28e-52
                540.00
76.88%
52.69%
48.87%
                                     Best Local Similarity:
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Alignment Scores:
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AlaLysGlnTyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyValGlyLys 21 ~

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Lung cancer associated gene sequences, referred to as lung cancer

reproductive; 141 AAGTGTGTGTGAATGACAAGAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCCCTC 466 GluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGluSer 161 PheThrArgLeuThrGluLeuValLeuGlnAlaHisArgLysGluLeuGluGlyLeuArg 181 121 286 82 GlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIleMetLys 101 GCGAAGACCTACGATTACCTGTTCAAGCTGCTGCTGATCGGGGACTCGGGGGTGGGGAAG 106 TrpAspThrAlaGlyGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArgAla 81 Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; cardioactive; phrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproduc proliferative disorder; wound healing; infectious disease; ds. TrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIleGlyAsn LysalaaspGluGluGlnLysargGlnValGlyArgGluGlnGlyGlnGlnLeuAlaLys 467 GACTATGGAATCAAGTTCATGGAGACCAGCGCGAAGGCCAACATCAATGTGGAAAATGCA GlyValAspPheLysMetLysThrIleGluValAspGlyIleLysValArgIleGlnIle 22 ThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSerThrIle Lung cancer associated polynucleotide sequence SEQ ID 91. AAF18072 standard; DNA; 1274 BP. GENOME SCI INC. 08-MAR-2000; 2000WO-US05918. MetArgAlaSerAsnGlu 187 ::: |||||||::: 587 CCCCAGGGGAGCAACCAG 604 (first entry) WPI; 2000-587514/55. (ROSE/) ROSEN C A. P-PSDB; AAB58196 WO200055180-A2. (HUMA-) HUMAN Homo sapiens. 12-MAR-1999; 21-SEP-2000. 14-MAR-2001 Ruben SM; AAF18072; 182 102 122 407 142 162 107 191 62 42 RESULT 7 AAF18072 g g g δ g Dp δ g ò Ωp δ g δ Dp δy ò δ

790

672 GGCAACAAGCCTCCCAGTACTGACCTGAAACTTGTGACAAGAAGAA-CACCAACAAGTG 730

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                                                                                           Sesociated proteins represented in AABS186. - AABS18548 Lung cancer associated proteins represented in AABS186. - AABS18548 Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and municular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18433 and peptide AABS8549 are used in the course of the invention for the peptide AABS8549 are used in the course of the invention for the lentification and characterisation of the polynucleotide and protein
useful for treatment, prevention, and diagnosis of disorders
                                                                                sequences AAF17982 - AAF18424 encode human lung cancer
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GCTTTTAGTTCCCTGGCCCGGGACATCTTGCTCAAGTCAGGAGGCCGGAGATCAGGAAAC
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                                                Page 566; 1425pp; English.
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This invention describes a novel human RablO cDNA sequence. The protein coded by said sequence belongs to Yap/Rab family and is the homolog of mouse RablO. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes the human RablO protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of human gene coding sequence, its encoded polypeptide
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197 GluGlyLysProGluGlyProAlaAsnSerSerLysThrCysTrp 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 716 BP; 226 A; 151 C; 182 G; 157 T; 0 other;
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                        791 AACGGCAGAGGGAGTGAGCAGGGGGAGAAATAGCAGAGGGGCTTGG
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Conservative:
Mismatches:
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                                                                                                                                                                          Human; Rab10; Yap/Rab family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 17; 23pp; Chinese.
                                                                         BP
                                                                         AAA40104 standard; cDNA; 716
                                                                                                                                                                                                                                                                          98CN-0121911.
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530.50
82.56%
55.81%
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                                                                                                                                                                                                    Homo sapiens
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This invention describes a novel human RablO cDNA sequence. The protein
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                                                                                                                                                                                                                                                                                                                                                ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile
                                                                                                                                    MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle
                                                                                                                                                                                                                                                               455 GGAAACAAGTGTGATATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAGAACAGATT
                                                                                                                                                                  GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                                                                                                                                                          ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
                                                                              GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
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                                                                                                                                                                                                                                                                                                                                                                               160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171
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Gaps:
                  (1-861)
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                   US-09-817-198A-2 (1-212) x AAA40108
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                                                                                                                                                                                          AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
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                                                                                                                     GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139
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                                    80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
                                                                             GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
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coded by said sequence belongs to Yap/Rab family and is the homolog of mouse Rabio. The present invention also relates to the polypeptide coded by said nucleotide sequence and the application and preparing process of said polynucleotide and said polypeptide. This sequence encodes a canine Rablo protein described in the method of the invention.
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                                                202 G; 223 T;
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                                               BP; 261 A; 202 C;
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Best Local Similarity:
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                                                              Alignment Scores:
Pred. No.:
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constitute the largest family of small Grpeases, with over 40 identified isoforms. RAB proteins contain four highly conserved peptide sequences involved in GTP binding and hydrolysis. Compositions comprising RAB nucleic acid are useful for identifying homologous or related genes, in producing compositions that modulate the expression or function of RAB, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, modulation of the gene activity in vivo is used for prophylactic and therapeutic purposes, such as treatment of cancer, and identification of cell type based on expression. The DNA may also be used to identify expression of
                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                protein useful for composition that
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                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes a mammalian RAB protein. RAB proteins
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                                                                                                                                                                                    AJ;
                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a mammalian RAB protein identifying homologous or related genes, in producing composimodulates expression or function of RAB for cancer therapy -
                                                                                                                                                                                    Buckler
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                                                                                                                                                                                    Vega
                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 38-39; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gene in a biological specimen.
                                                                                                                                                                                    McIntosh B,
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530.50
82.56%
55.81%
                                           13-MAR-2000; 2000WO-US06330
                                                                                        99US-0126083
                                                                                                                                    (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                             2000-647233/62
                                                                                                                                                                                    Abel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                        25-MAR-1999;
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05-OCT-2000
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RESULT 12 AAF16196 ID AAF1

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primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                                                                                                                                                                                                100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle
                                                                                                                                                                                                                                                                                                                 80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle
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833 AGCAAATGGCTIAGAACAIGAGGATGACCCAAIGAAGAIGTGGAAAGAAGAATGTIACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlnGlnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          893 GGAAACAAGTGTGATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAGAACAGATT
                                                                                                                                                                                                                                                                                               GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg
                                                                   1 MetAlaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal
                                                                                                                                           20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1013 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 1048
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, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171
                                   US-09-817-198A-2 (1-212) x AAF16196 (1-1537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:17618
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaccological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                          prostate cancer; prostate cancer antigen; detection; diagnosis;
                     140 AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159
                                         Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                           Human prostate cancer antigen nucleotide sequence SEQ ID NO:631.
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                      160 GluSerPheThrArgLeuThrGluLeuValLeuGln
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                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                AAF16196 standard; cDNA; 1537
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530.50
82.56%
55.81%
48.01%
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P-PSDB; AAB56993.
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Best Local Similarity:
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Saito K, Ya , Otsuki T;

Pred. No.:

بر د

832 119 892

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772

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs

160 GluSerPheThrArgLeuThrGluLeuValLeuGln 171

Claim 8; SEQ ID 17618; 2537pp + CD ROM; English.

full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asaily without any specialised methods. AAH03166 to AAH13632 to AAH13632 to AAH13633 to AAH3632 to AAH3632 to AAH3632 to AAH3632 to AAH36332 of the process the used in the exemplification of the process. present invention describes primer sets for synthesising 5602 the present invention

Sequence 3533 BP; 967 A; 716 C; 730 G; 1120 T; 0 other;

740 GGCGCAATGGGTATCATGCTAGTATATGACATCACCAATGGTAAAAGTTTTGAAAACATC 799 GlyAsnLysAlaAspGluGluGlnLysArgGlnValGlyArgGluGlnGlyGlnGlnLeu 139 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer 39 MetAlaLysGln---TyrAspValLeuPheArgLeuLeuLeuIleGlyAspSerGlyVal 19 100 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 40 ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgile 80 ArgAlaGlnGlyIlePheLeuValTyrAspIleSerSerGluArgSerTyrGlnHisIle GGAAACAAGTGTGATATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAGAACAGATT GlnIleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArg 3533 96 46 29 1 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-817-198A-2 (1-212) x AAH17889 (1-3533) 4.85e-51 530.50 82.56% 55.81% 48.01% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: 7 20 120 140 9 ò 셤 ö a à qq qq ò 염 ò g ò ద à ö

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619

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Indels:

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AlaLysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLys 159

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in esponsible for genetic disorders or other traits to assess biodiversity Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity BP; 218 A; 136 C; 173 G; 147 T; 0 other; 674 96 129 129 DNA encoding novel human diagnostic protein #7257 Matches: Conservative: Mismatches: 980 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 1015 at ftp.wipo.int/pub/published_pct_sequences Claim 1; SEQ ID No 7257; 103pp; English. Tang YT; AAS71453 standard; cDNA; 674 6.62e-52 529.50 82.56% 55.81% 2000US-0540217. 2000US-0649167. 30-MAR-2001; 2001WO-US08631 13-FEB-2002 (first entry) 2001-639362/73. Drmanac RT, Liu C, Percent Similarity: Best Local Similarity: Query Match: (HYSE-) HYSEQ INC P-PSDB; ABG07266 WO200175067-A2. Sequence 674 Homo sapiens. biodiversity 31-MAR-2000; 23-AUG-2000; 11-OCT-2001. AAS71453; RESULT 14 g

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LysGluTyrGlyMetAspPheTyrGluThrSerAlaCysThrAsnLeuAsnIleLysGlu 160
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Human; G-protein; 32705; 23224; 27423; 32700; 32712; lung disorder; congenital anomaly; pulmonary congestion; oedema; haemorrhage; adult respiratory distress syndrome; Goodpasture's syndrome; chronic obstructive pulmonary disease; asthma; pulmonary hypertension; liver disorder; hepatic injury; jaundice; cholestasis; viral hepatitis; cirrhosis; Wilson's disease; autoimmune hepatitis; hepatic failure; brain disorder; hypoxia; cerebral ischemia; intracranial hemorrhage; acute meningitis; Parkinson's disease; Alzheimer's disease; glioma; chronic bacterial meningeoncephalitis; multiple sclerosis;
                                                                                                                                                                                                 MetLysTrpValSerAspValAspGluTyrAlaProGluGlyValGlnLysIleLeuIle 119
                                                                                                                                                                                                                                                            434
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                                                MetAlaLysGln---TyrAspValLeuPheArgLeuLeuLleGlyAspSerGlyVal
                                                                              20 GlyLysThrCysLeuLeuCysArgPheThrAspAsnGluPheHisSerSerHisIleSer
                                                                                         435 GGAAACAAGTGTGATATGGACGACAAAAGAGTTGTACCTAAAGGAAAAGGAAACAGATT
                                                                                                                     40 ThrileGlyValAspPheLysMetLysThrileGluValAspGlyIleLysValArgIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amyotropic lateral sclerosis; stroke; Huntington's disease; ss
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                                                                                                                                                                                                                                                                                                                                                                                 555 AAGGCGTTCCTCACGTTAGCTGAAGATATCCTTCGA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of human 27423 G-protein.
  Gaps:
                   US-09-817-198A-2 (1-212) x AAS71453 (1-674)
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The present sequence encodes a human G-protein. The specification describes 32705, 23224, 27423, 32700 or 32712 small G-proteins. The Gescribes 32705, 23224, 27423, 32700 or 32712 small G-proteins. The G-protein polypeptides and polynucleotides are useful as a target for diagnosis and treatment of G-protein mediated or related disorders, and for identifying agonists and antagonists for diagnosis and treatment. They are useful for treating disorders of lung (e.g. congenital anomalies, pulmonary congestion, oedema, adult respiratory distress syndrome, haemorrhage, chronic obstructive pulmonary disease, asthma, Goodpasture's syndrome and pulmonary hypertension), liver (e.g. hepatic injury, jaundice, cholestasis, viral hepatitis, cirrhosis, brain (e.g. hypoxia, cerebral ischemia, intraoranial haemorrhage, acute meningitis, Parkinson's disease, Alzheimer's disease, gllomas, chronic bacterial meningoencephalitis, multiple sclerosis, amyotropic lateral selections and selective and funtington's disease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleTrpAspThrAlaGlyGlnGluArgTyrGlnThrIleThrLysGlnTyrTyrArgArg
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                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                     Novel human small G-protein polypeptides and polynucleotides treating lung disorders, liver disorders and brain disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1161 BP; 368 A; 246 C; 243 G; 304 T; 0 other;
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Matches:
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                                                  (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.81e-51
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                                                                                                                                                                                                  P-PSDB; AAG67154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
29-FEB-2000;
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Search completed: November 17, 2002, 20:47:19 Job time : 260 secs

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Sequence 5, Appli
Sequence 534, Appli
Sequence 1571, Ap
Sequence 6, Appli
Sequence 766, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 16, Appli
                                                                                                                (without alignments)
159.645 Million cell updates/sec
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                                                                                                                                                                                            1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC
                                                                                          November 17, 2002, 20:38:29 ; Search time 20 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-817-198A-5
US-09-917-198A-4
US-09-925-302-5-34
US-09-925-30-1571
US-09-925-30-1571
US-09-927-86-5
US-09-834-765-76
US-09-967-736-8
US-09-981-7-1998-7
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Maximum Match 100%
Listing first 45 summaries
                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 3, Appli
Sequence 1077, Ap
Sequence 5, Appli
Sequence 762, Appli
Sequence 763, Appli
Sequence 763, Appli
Sequence 10, Appli
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Sequence 6, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 764, Appli
Sequence 4, Appli
Sequence 764, Appli
Sequence 764, Appli
Sequence 112, Ap
Sequence 1812, Ap
Sequence 6, Appli
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Sequence 1812, Ap
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                                                                                                                                                                                                                                                           Sequence 2, Application US/09817198A
Patent No. US20020146758A1
GENERAL INFORMATION
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NCCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REPERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT APPLICATION NUMBER: US/09/817,198A
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1105; DB 10; Length 212; Lilarity 100.0%; Pred. No. 1.2e-102; Conservative 0; Mismatches 0; Indels 0;
                                                                                 0.52-10-108-605-45
0.05-10-108-605-45
0.05-09-945-173-10
0.05-09-925-300-1364
0.05-09-820-003A-2
0.05-10-051-986-1
0.05-09-820-003A-2
0.05-10-051-986-1
0.05-09-814-765-764
0.05-09-814-765-764
0.05-09-814-761-42996
0.05-09-988-974-9
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0.05-09-988-974-9
US-09-925-302-783
US-09-794-257-5
US-09-988-974-8
US-09-925-301-1077
US-09-925-301-1077
US-09-834-765-2
US-09-834-765-762
US-09-834-765-765
US-09-834-765-765
US-09-834-765-765
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ses 212; Conserv
 ORGANISM: Human
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US-09-817-198A-2
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LENGTH: 212
 TYPE: PRT
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7 RESULT

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181 RMRASNELALAELEEEEGKPEGPANSSKTC 210
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                                                                                                                                                           Sequence 534, Application US/09925302 Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-925-302-534
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Best Local Similarity
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US-09-925-302-534
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LENGTH: 246
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Patent NO. US20020146758A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: NOCIEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REPERENCE: CLO01188
CURRENT APPLICATION NUMBER: US/09/817,198A
CURRENT APPLICATION NUMBER: US/09/817,198A
SOFTWARE: FastSEQ for Windows Version 4.0
                                          GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

FILE REFERENCE: CL001188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FASTERQ for Windows Version 4.0

SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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Pred. No. 2.4e-101;
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            Sequence 5, Application US/09817198A Patent No. US20020146758A1
                                                                                                                                                                                                                                                                                                                         Query Match 98.8%;
Best Local Similarity 97.2%;
Matches 212; Conservative
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                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
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TYPE: PRT
US-09-817-198A-5
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121 NKÅDEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 MAKAYDHLFKILLIGDSGVGKTCLIIRFAEDNFNNTYISTIGIDFKIRTVDIEGKKIKILQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFRENCE: PA101
CURRENT FILING DATE: 2001-08-10
FRICH APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
FRIOR FILING DATE: 2000-03-08
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PAtentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 246;
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
NUCLEIC Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
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Best Local Similarity 47.6%; Pred. No. 1.3e-45;
Matches 100; Conservative 49; Mismatches 43;
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Gaps

8;

Indels

42;

Length 190;

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46.3%; Score 512; DB 10;
47.7%; Pred. No. 8.8e-44;
tive 52; Mismatches 42;
ORGANISM: Discopyge ommata
                                                                                         93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-834-765-766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-967-736-3
     ; ORGANISM. US-09-822-860-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                           186
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                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-794-257-8
Sequence 8, Application US/09794257
Sequence 8, Application US/09794257
Sequence 8, Application US/09794257
Seturn No. US2002009804A1
GENERAL INFORMATION:
APPLICANT MEYERS, Rachel
TITLE OF INVENTION: 4 Human G-Proteins
TITLE OF INVENTION: Human G-Proteins
TITLE OF INVENTION: 400-200-200-200
CURRENT APPLICATION NUMBER: US/09/794,257
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: ZHU, Shiaoping et al.
APPLICANT: ZHU, Shiaoping et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO01214
CURRENT APPLICATION NUMBER: US/09/822,860
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 190
TYPE: PRT
                                                                                                                                                                  60 QIWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILI 119
                                                                                                                                                                                   61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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                                                      Gaps
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                                                                                         1 MAKQ-YDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRI 59
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                 DB 10; Length 218;
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                                                      Indels
               48.0%; Score 530.5; DB 10; 55.8%; Pred. No. 1.5e-45; live 46; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.8%; Score 528.5; DB 1
Best Local Similarity 54.0%; Pred. No. 2.3e-45;
Matches 95; Conservative 47; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/09822860
; Patent No. US20020146795A1
                                 Local Similarity 55.89 ies 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: homo sapiens
US-09-794-257-8
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LENGTH: 207
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                                                    Matches
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                                                                                                                                                                                                                                                                                66 GQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIGNKADE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 EQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGLRMRAS 185
                                                                            6 DVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDTA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 FRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDTAGQE 68
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Fatent No. US20020055478a1
GENERAL INFORMATION:
APPLICANT: MANY Fais
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Daniel E.H. Afar
APPLICANT: Daniel E.H. Afar
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: AND DETECTION OF CANCER
FILE REFERENCE: 129.60GU1
CURRENT APPLICATION NUMBER: US/09/834,765
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 4, Application US/09820003A

Sequence 4, Application US/09820003A

Patent No. US20020142382A1

GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISCLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REPERENCE: CLOOI196

CURRENT APPLICATION NUMBER: US/09/820,003A

CURRENT FILING DATE: 2001-03-29

NUMBER O'SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGHH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.4%; Score 469; DB 10;
Best Local Similarity 51.2%; Pred. No. 1.8e-39;
Matches 83; Conservative 36; Mismatches 43;
                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                             ATTORNEY ACENTION NUMBER: 09/154,602
FILING DATE: <UNKNOWN>
NAME: SILIINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 201 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
CLONE: 57006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear IMMEDIATE SOURCE:
NUMBER OF SEQUENCES:
                                                          STREET: 3174 POI
                                                                                                                    USA
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ORGANISM: Homo sapien
                                                                                                                      COUNTRY:
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US-09-820-003A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.0%; Pred. No. 2e-40;
Matches 91; Conservative 42; Mismatches 64; Indels 5;
                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/967,736
FILING DATE: 28-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/154,602
FILING DATE: CURKNOWN>
ATORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0367 US

TELECOMMUNICATION INFORMATION:

TELEFRAN: 415-845-055

TELEFRAX: 415-845-055
                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-967-736-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
          Lal, Preeti
Corley, Neil C.
Shah, Purvi
TITLE OF INVENTION: RAB PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09967736 Patent No. US20020103340A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 201 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 RMRASNELALAELEEEEGKPEG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 GAASGERPNLKIDSTPVKPAG 197
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: LIVRTUT04
CLONE: 2514506
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                              ZIP: 94304
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SOFTWARE: Fast
SEQ ID NO 5
LENGTH: 198
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US-09-972-529-4
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                                                                TYPE: PRT
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                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09794257
Patent No. US200200980441
APPLICANT: Nevers, Rachel
TITLE OF INVENTION: 32705, 23224, 27423, 32700, 32712, No. US20020009804Alel
TITLE OF INVENTION: Human G-Proteins
FILE REFERBNCE: 35800/209285
CURRENT FILLIG DATE: 2001-02-27
PRIOR PILLING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
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                                                                                                                                                                                 70 YQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYA--PEGVQKILIGNKAD--- 124
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 RLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQIWDTAGQER 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 -----EEQKRQVGREQGQQLAKEYG-MDFYETSACTNLNIKESFTRLTELVLQ 171
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Patent No. US20020127568A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 47324, A NOVEL HUMAN G-PROTEIN AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 38155-20035.00
CURRENT APPLICATION NUMBER: US/09/945,173
CURRENT APPLICATION NUMBER: 05.001-08-31

PRIOR FILING DATE: 2000-09-01
                                  Length 222;
                              42.3%; Score 467; DB 10; Length 251.9%; Pred. No. 3.2e-39; Live 34; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                  121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Pfam accession number PF00071
US-09-794-257-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 16
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                             Query Match
Best Local Similarity 51.9
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 89; Conserv
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US-09-820-003A-4
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US-09-945-173-5
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70 YQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYA--PEGVQKILIGNKAD--- 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 -----EEQKRQVGREQGQLAKEYG-MDFYETSACTNLNIKESFTRLTELVLQ 171
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                                                                                                                                                                                                                                                        Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09972529
Fatent No. US20020150916A1
GENERAL INFORMATION:
APPLICANT: Mileonium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 47316, A NOVEL HUMAN G-PROTEIN AND USES
TITLE OF INVENTION: 47316, A NOVEL HUMAN G-PROTEIN AND USES
TITLE OF INVENTION: 47316, A NOVEL HUMAN G-PROTEIN AND USES
TITLE OF INVENTION: 47315. 20041.00
CURRENT APPLICATION NUMBER: US/09/972,529
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/237,716
FILING DATE: 200-10-05
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-972-529-4
                                                                                                                                                                           ; OTHER INFORMATION: Consensus amino acid sequence US-09-945-173-5
                                                                                                                                                                                                                                                     ; Score 434.5; DB 10; Pred. No. 4.7e-36; 30; Mismatches 43
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 4, Application US/09817199A
; Patent No. US20020142380A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     Query Match 39.3%;
Best Local Similarity 50.9%;
                                                                                                                            ORGANISM: Artificial Sequence
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Matches 89; Conserv
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## APPLICANT: SHAO, Wei et al.
### TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
### TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
### TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
### CURRENT APPLICATION NUMBER: US/09/817,199A

### CURRENT APPLICATION NUMBER: US/09/817,199A

### CURRENT APPLICATION NUMBER: US/09/817,199A

### CURRENT FILLE DATE: 2001-03-27

### NUMBER OF SEQ ID NOS: 25

### SEQ ID NO 4

### CORALISM: Mus musculus

### CORALISM: Musculus

### CORALISM:
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